

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2004, 00:22:53 ; Search time 9711.65 Seconds  
(without alignments)  
12622.391 Million cell updates/sec

Title: US-09-931-157-1  
Perfect score: 4105  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result			%				DB	ID	Description
	No.	Score	Match	Length	Query				
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	2	1074.6	26.2	1284	29	AY417817		AY417817	Pan trogl
	3	1069	26.0	3538	11	AK043210		AK043210	Mus muscu
	4	862.2	21.0	1284	29	AY417818		AY417818	Mus muscu
	5	797.8	19.4	865	9	AU118882		AU118882	AU118882
	6	792.2	19.3	863	9	AU119546		AU119546	AU119546
	7	789	19.2	869	9	AU120519		AU120519	AU120519
	8	752.2	18.3	783	13	BX109539		BX109539	BX109539
	9	750.6	18.3	3150	11	AK042211		AK042211	Mus muscu
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	11	710.4	17.3	733	12	BM719244		BM719244	UI-E-EO1-
c	12	704.2	17.2	777	12	BQ018994		BQ018994	UI-H-DH1-
	13	695.8	17.0	764	9	AU139639		AU139639	AU139639
	14	694.8	16.9	782	14	CD246193		CD246193	AGENCOURT
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c	21	681.4	16.6	703	13	BU681421		BU681421	UI-CF-EC1
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c	23	661	16.1	661	13	BU948045		BU948045	io49d10.x
c	24	653.4	15.9	724	9	AI953824		AI953824	wx69h09.x
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	34	609.4	14.8	978	14	CD359210		CD359210	AGENCOURT
	35	603.2	14.7	1043	12	BG114663		BG114663	602315469
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## ALIGNMENTS

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 LOCUS AY417816 1284 bp DNA linear GSS 17-DEC-2003  
 DEFINITION Homo sapiens EDNRA gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 ACCESSION AY417816  
 VERSION AY417816.1 GI:39773776  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1284)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 1284)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
 FEATURES Location/Qualifiers  
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 /mol\_type="genomic DNA"  
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 Best Local Similarity 87.9%; Pred. No. 6.2e-240;  
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 Db 1 ATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT 60  
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Db	121	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	180
Qy	665	AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAAA	724
Db	181	AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAAA	240
Qy	725	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACT	784
Db	241	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACT	300
Qy	785	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
Db	301	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	360
Qy	845	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
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Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
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Qy	965	TTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	481	TTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	540
Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGAATTGGGATTCCTTTG	1084
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Qy	1085	GTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCTTGAA	1144
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Db	661	GCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	720
Qy	1205	CTCAATGCCACATCAAATTCATGGAGTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
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Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1324
Db	781	NN	840
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384
Db	841	NN	900
Qy	1385	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGCTGGTTC	1444
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 Qy 1745 AGCCATAAGGACAGCATGAACTGA 1768  
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 Db 1261 AGCCATAAGGACAGCATGAACTGA 1284

## RESULT 2

AY417817

LOCUS AY417817 1284 bp DNA linear GSS 17-DEC-2003

DEFINITION Pan troglodytes EDNRA gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY417817

VERSION AY417817.1 GI:39773777

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 1284)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1284)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

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Qy	1205	CTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	721	CTCAATGCCACATCAAATTCATGGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	780
Qy	1265	GGTTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1324
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Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384
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Qy	1385	CGTCGAGAAGTGGCAAAAACAGTTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTC	1444
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Db	1261	AGCCATAAGGACAGCATGAACTGA	1284

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

- Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
- REFERENCE 1  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636
- REFERENCE 2  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159
- REFERENCE 3  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861
- REFERENCE 4  
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)
- REFERENCE 5  
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)
- REFERENCE 6 (bases 1 to 3538)  
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.go.jp/  
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers  
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/note="unnamed protein product; SIMILAR TO ENDOTHELIN  
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SLMTSVPMNGTSIQWKNQEQQNNHNTERSSSHKDSMN"

ORIGIN

Query Match 26.0%; Score 1069; DB 11; Length 3538;  
Best Local Similarity 73.9%; Pred. No. 7.8e-227;  
Matches 1501; Conservative 0; Mismatches 470; Indels 60; Gaps 9;

Qy 140 CCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATCCATCCCACCCGGTCG 199  
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Db 5 CCTTCTAGTCTGGCAACTGTGTCTAGGAGGTGGGGAGCCTCTCTCTGATCCACCGGACCA 64  
Qy 200 TCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAGTGCCCGAGGAAGTTT 259  
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Db 65 TCGCTGGAGCTTGCGAGGCTGAGCAAGATCTCCC-----CCTAGAGAAGCCT 110  
Qy 260 CTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGAGCCCGGGACACCGGC 319  
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Db 111 GGCTGTCCGGGGAAGTT----TCCCCGAGCTGAGACTGTGCTGCAGCCCTGGTCACCCGC 166

Qy	320	CACCCCTCCGCGCCACCCACCCTCGCTTTCTCCGGTTCTCTTGCCCCAGGCGCCGCGCGG	379
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Db	221		
		GACCTGGAGCTGTCTGCTTCCGAGGAGCTCTAAGGTGAAAAAAGAAAGGCGTGAGACCA	280
Qy	440	GCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAGATGGAAACCCTTTGC	499
Db	281		
		ACATAAGAAG-----ACTTAAATCCAGGTTAAGATGAGTATCTTTTGC	324
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Db	385		
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Qy	620	AGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCCAGCAATGGCTCAATG	679
Db	445		
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Qy	680	CACAACTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTG	739
Db	505		
		CACGGCTATTGCCCACAGCAGACTAAAATCACGACAGCTTCAAATATATTAACACTGTG	564
Qy	740	ATATCTTGTAATTTTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATT	799
Db	565		
		ATATCCTGCACCATTTTCATCGTGGGAATGGTGGGGAACGCAACTCTACTACGAATCATT	624
Qy	800	TACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGA	859
Db	625		
		TACCAAAACAAGTGTATGAGGAACGGCCCCAATGCCTCATAGCCAGCCTGGCCCTTGGA	684
Qy	860	GACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGC	919
Db	685		
		GACCTTATCTACGTGGTCATTGACCTCCCATCAACGTGTTAAGCTCTTGACAGGACGC	744
Qy	920	TGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTCGAG	979
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		TGGCCTTTTCGACCACAATGATTTTGGAGTGTCTCTGCAAGCTGTTCCCTTCCTGCAG	804
Qy	980	AAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGA	1039
Db	805		
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Db	865		
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Qy	1100	ATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTC	1159
Db	925		
		ATCGTCTCCATCTGGATTCTTTCCTTCATCTTGGCCATCCCGGAAGCAATCGGCTTCGTC	984
Qy	1160	ATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCCACATCA	1219

Db	985		ATGGTACCCTTCGAATACAAGGGCGAGCTGCATAGGACCTGCATGCTCAACGCCACGTCC	1044
Qy	1220		AAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTCTATTTCTGT	1279
Db	1045		AAGTTCATGGAGTTTTACCAAGATGTGAAGGACTGGTGGCTCTTTGGGTCTACTTCTGC	1104
Qy	1280		ATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGA	1339
Db	1105		ATGCCCTTGGTGTGCACAGCAATCTTCTACACCCTCATGACCTGTGAGATGCTCAACAGG	1164
Qy	1340		AGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCA	1399
Db	1165		AGGAACGGCAGCTTGC GGATCGCCCTTAGTGAGCACCTCAAACAGCGTCGAGAAGTGGCA	1224
Qy	1400		AAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGC	1459
Db	1225		AAGACTGTCTTCTGCTTGGTTGTCATCTTCGCCCTGTGCTGGTTCCTCTTCACTTAAGC	1284
Qy	1460		CGTATATTGAAGAAAACGTGTGATAACGAAATGGACAAGAACCGATGTGAATTACTTAGT	1519
Db	1285		CGCATTTTGAAGAAAACGTATATGATGAGATGGATAAGAACCGGTGTGAAGTCTCAGC	1344
Qy	1520		TTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAAC	1579
Db	1345		TTCTTGCTGCTAATGGATTACATCGGCATTAACCTGGCAACCATGAATTCCTGCATAAAC	1404
Qy	1580		CCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGC	1639
Db	1405		CCAATAGCTCTATATTTTGTGAGCAAGAAATTCAAAAATTGTTTTCAGTCCTGCCTCTGT	1464
Qy	1640		TGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATGAACGGAACAAGCATC	1699
Db	1465		TGCTGTTGTCAACAGTCCAAAAGCCTCATGACCTCGGTCCCCATGAATGGAACGAGTATC	1524
Qy	1700		CAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGC	1759
Db	1525		CAGTGGAAGAACCAAGAGCAGAACAACCACAACACGGAACGGAGCAGCCACAAGGACAGC	1584
Qy	1760		ATGAACTGACCACCTTAGAAGCACTCCTCGGTACTCCCATAATCCTCTCGGAGAAAAAA	1819
Db	1585		ATGAACTAACCCTCCGCAGAAACACCGAGACGTGTGCCTTCAAGTCCTAGGATGGAACA	1644
Qy	1820		ATCACAAGGCAACTGTGACTCCGGGAATCTCT-----TCTCTGATCCTTCTTCCTTA	1871
Db	1645		ACCATTACGCCACAGATGCGCTCCCAAACCTCCCAAGTCTCTCCCATGCTCCTTTTCTA	1704
Qy	1872		ATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGGTTTATCC	1931
Db	1705		AGTCCATCCTAGGAAAAGCTCTCCTGCCCTCCCAACAGCACGTGGTGGACCGGT-----C	1759
Qy	1932		ACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCTGCGTGT	1991
Db	1760		CCAGCTATAGCCAATGGGTCTTTCCTGAGTACTGTATATGATTTGCATACCGCGCATGTC	1819
Qy	1992		GTATTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCA	2051

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Db      1820 ATTTCCAACACTTGAAAAT-----TAGAGCTGGGAGAAAGGAGA-TGATGGTTCAAAGAA 1873
Qy      2052 GAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTAT 2111
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Db      1874 GCCACCTAGCTGCCGCCTTTGCATGAACACAGAGTTTGCAAGTTCATGACCAGCTTCCGT 1933
Qy      2112 GGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAG 2162
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Db      1934 -GCAGTTCTATGGACCAGCTGGTGGGAACTGTCCATCCTAAGATTCTAGAG 1983

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RESULT 4

AY417818

LOCUS AY417818 1284 bp DNA linear GSS 17-DEC-2003

DEFINITION Mus musculus EDNRA gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY417818

VERSION AY417818.1 GI:39773778

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1284)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1284)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

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source      1..1284
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gene        <1..>1284
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ORIGIN

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Query Match      21.0%; Score 862.2; DB 29; Length 1284;
Best Local Similarity 75.0%; Pred. No. 8e-181;
Matches 963; Conservative 0; Mismatches 321; Indels 0; Gaps 0;

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Qy 485 ATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT 544



Db	1	ATGAGTATCTTTTGCCTTGCGGCATACTTTTGGCTGACCATGGTGGGAGGCGTAATGGCT	60
Qy	545	GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCACCTTTT	604
Db	61	GACAATCCGGAGAGATACAGCGCTAATCTAAGCAGCCACATGGAAGACTTCACCCCTTTT	120
Qy	605	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	664
Db	121	CCGGGGACGGAGATCAACTTTCTGGGCACCACCCATCGACCCCTAATTTGGCCCTGCCT	180
Qy	665	AGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAA	724
Db	181	AGCAATGGCTCAATGCACGGCTATTGCCCACAGCAGACTAAAATCACGACAGCTTTCAA	240
Qy	725	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGCAACT	784
Db	241	TATATTAACACTGTGATATCCTGCACCATTTTCATCGTGGGAATGGTGGGAACGCAACT	300
Qy	785	CTGCTCAGGATCATTTACCAGAACAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
Db	301	CTACTACGAATCATTTACCAAAACAAGTGTATGAGGAACGGCCCCAATGCGCTCATAGCC	360
Qy	845	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	361	AGCCTGGCCCTTGGAGACCTTATCTACGTGGTCATTGACCTCCCATCAACGTGTTTAAG	420
Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
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Qy	965	TTCCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	481	TTCCCCCTTCTGAGAAGTCCTCCGTGGGCATCACCGTCTTGAACCTCTGTGCTCTCAGT	540
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Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
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Qy	1265	GGGTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1324
Db	781	NN	840
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384



Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES                      Location/Qualifiers  
    source                      1. .865  
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ORIGIN

Query Match                      19.4%;    Score 797.8;    DB 9;    Length 865;  
Best Local Similarity            98.0%;    Pred. No. 1.7e-166;  
Matches 847;    Conservative    0;    Mismatches    12;    Indels        5;    Gaps        4;

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Db	61	ACATCGGTATTAACCTTGGCAACCATGAATTCATGTATAAACCCCATAGCTCTGTATTTTG	120
Qy	1599	TGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCA	1658
Db	121	TGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCA	180
Qy	1659	AAAGTCTGATGACCTCGGTCCCCATGAACGGAACAAGCATCCAGTGGAAGAACCACGATC	1718
Db	181	AAAGTCTGATGACCTCGGTCCCCATGAACGGAACAAGCATCCAGTGGAAGAACCACGATC	240
Qy	1719	AAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAG	1778
Db	241	AAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAG	300
Qy	1779	AAGCACTCCTCGGTACTCCCATAACTCTCTCGGAGAAAAAATCACAAGGCAACTGTGAC	1838
Db	301	AAGCACTCCTCGGTACTCCCATAACTCTCTCGGAGAAAAAATCACAAGGCAACTGTGAC	360
Qy	1839	TCCGGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATG	1898
Db	361	TCCGGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATG	420
Qy	1899	CTTTCCAAAACCGCAA-GGTAGACTGGTTTATCCACCCACAACATCTACGAATCGTACTT	1957
Db	421	CTTTCCAAAACCGCAAGGGTAGACTGGTTTATCCACCCACAACATCTACGAATCGTACTT	480
Qy	1958	CTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGA	2017
Db	481	CTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGA	540
Qy	2018	GCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTTTTGCATGA	2077

Db 541 GCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTTTTGCATGA 600  
 Qy 2078 AAATAGAGCTTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGG 2137  
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 Db 601 AAATAGAGCTTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGG 660  
 Qy 2138 AACTGGTCACCATGAAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGA- 2196  
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 Db 661 AACTGGTCACCATGAAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGAT 720  
 Qy 2197 TTTTTTGTCTTCAGCCAAACACAATATGGGCTCAGGTCACTTTTATTTGAAATGTCATT 2256  
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 Db 721 TTTTTTGNCCTTCAGCCAAACACAATATGGGCTCAAGTCACTTTTATTTGAAATGNCATT 780  
 Qy 2257 TGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATG--ATTATTTGAACTTATTTA- 2313  
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 Db 781 TGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGGATTATTTGGAACTTATTTAC 840  
 Qy 2314 CACATAGTTTGAAAAAAAAAAGAC 2337  
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 Db 841 CNCNTAGTTTGAAAAAAAAAAGAC 864

# RESULT 6

AU119546

LOCUS AU119546 863 bp mRNA linear EST 01-AUG-2002

DEFINITION AU119546 HEMBA1 Homo sapiens cDNA clone HEMBA1006071 5', mRNA sequence.

ACCESSION AU119546

VERSION AU119546.1 GI:10934781

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 863)

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project

JOURNAL Unpublished (2000)

COMMENT Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES Location/Qualifiers

source 1. .863

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="HEMBA1006071"  
/tissue\_type="whole embryo, mainly head"  
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/clone\_lib="HEMBA1"  
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ORIGIN

Query Match 19.3%; Score 792.2; DB 9; Length 863;  
Best Local Similarity 97.8%; Pred. No. 3e-165;  
Matches 845; Conservative 0; Mismatches 14; Indels 5; Gaps 4;

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Qy	2105	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGAT	2164
Db	61	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGAT	120
Qy	2165	TAACGACAAGATTTTCTACTTTTTTTAAGTGA--TTTTTTGTCTTCAGCCAAACACAAT	2222
Db	121	TAACGACAAGATTTTCTACTTTTTTTAAGTGA--TTTTTTGTCTTCAGCCAAACACAAT	180
Qy	2223	ATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTGCATA	2282
Db	181	ATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTGCATA	240
Qy	2283	ATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAAAA	2342
Db	241	ATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTG-AAAAAAAAGACAAAAA	299
Qy	2343	TAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTAAAAC	2402
Db	300	TAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTGTTTATTTTTTAAAAC	359
Qy	2403	ACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATT	2462
Db	360	ACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATT	419
Qy	2463	TGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAAT	2522
Db	420	TGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAAT	479
Qy	2523	GGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTT	2582
Db	480	GGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTT	539
Qy	2583	CAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAA	2642
Db	540	CAATCAGATAGTTCTTTTTTACAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAA	598
Qy	2643	AATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTC	2702
Db	599	AATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTC	658
Qy	2703	AGTGCACCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGAT	2762

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Db      659 AGTGCACCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGAT 718
Qy      2763 GATTTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCA 2822
        ||||| ||||||||||||||||||||||||||||||||||||||| |||||||||
Db      719 GATTTCAGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGNATATACATATCA 778
Qy      2823 CCTCCTATTCTCTTAATTTTTTGTAAATGTTAACTGGCAGT-AAGTCTTTTTTGATCAT 2881
        ||||||||||||||||||| ||||||| ||||||||| ||| ||||||||| |||
Db      779 CCTCCTATTCTCTTAATTTTTTCTTAAATGGTAACTGGCAGTAAAGCCTTTTTTGACCAT 838
Qy      2882 TCCCTTTTCCATATAGGAAACATA 2905
        ||||||||| | |||||| ||
Db      839 TCCCTTTTCATTTAGGGAAACTTA 862

```

# RESULT 7

AU120519

LOCUS AU120519 869 bp mRNA linear EST 01-AUG-2002

DEFINITION AU120519 HEMBB1 Homo sapiens cDNA clone HEMBB1000846 5', mRNA sequence.

ACCESSION AU120519

VERSION AU120519.1 GI:10935754

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 869)

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project

JOURNAL Unpublished (2000)

COMMENT Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

## FEATURES

source

Location/Qualifiers

1. .869

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="HEMBB1000846"

/tissue\_type="whole embryo, mainly body"

/dev\_stage="embryo, 10 weeks"

/clone\_lib="HEMBB1"

/note="Vector: pME18SFL3"

## ORIGIN

Query Match

19.2%; Score 789; DB 9; Length 869;

Best Local Similarity 98.0%; Pred. No. 1.5e-164;  
Matches 850; Conservative 0; Mismatches 12; Indels 5; Gaps 5;

Qy	1771	ACCCTTAGAAGCACTCCTCGGTACTCCCATATCCTCTCGGAGAAAAAATCACAAGGCA	1830
Db	1	ACCCTTAGAAGCACTCCTCGGTACTCCCATATCCTCTCGGAGAAAAAATCACAAGGCA	60
Qy	1831	ACTGTGACTCCGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCACCTCCACACCCAAG	1890
Db	61	ACTGTGAGTCCGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCACCTCCACACCCAAG	120
Qy	1891	AAGAAATGCTTTCCAAAACCGCAA-GGTAGACTGGTTTATCCACCCACAACATCTACGAA	1949
Db	121	AAGAAATGCTTTCCAAAACCGCAAGGGTAGACTGGTTTATCCACCCACAACATCTACGAA	180
Qy	1950	TCGTACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTTCAGCACTAAAAAA	2009
Db	181	TCGTACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTTCAGCACTAAAAAA	240
Qy	2010	TGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTT	2069
Db	241	TGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTT	300
Qy	2070	TTGCATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGT	2129
Db	301	TTGCATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGT	360
Qy	2130	TCAATGGGAAGTGGTCACCATGAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTT	2189
Db	361	TCAATGGGAAGTGGTCACCATGAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTT	420
Qy	2190	TAAGTGA-TTTTTTGTCTTCAGCCAAACACAATATGGGCTCAGGTCACCTTTTATTTGAA	2248
Db	421	TAAGTGATTTTTTTGTCTTCAGCCAAACACAATATGGGCTCAAGTCACCTTTTATTTGAA	480
Qy	2249	ATGTCATTTGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGATTATTTGAACCT	2308
Db	481	ATGTCATTTGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGATTATTTGAACCT	540
Qy	2309	ATTTACACATAGTTTGAAAAAAAAGACAAAAATAGTATTCAGGTGAGCAATTAGATTA	2368
Db	541	ATTTACACATAGTTTGAAAAAAAAGACAAAAATAGTATTCAGGTGAGCAATTAGATTA	600
Qy	2369	GTATTTTCCACGTCACTATTTATTTTTTTAAACACAAATCTAAAGCTACAACAAATAC	2428
Db	601	GTATTTTCCACGTCACTGGTTATTTTTTTAAACACANATTCTAAAGCTACAACAAATAC	660
Qy	2429	TACAGGCCCTTAAAGCACAGTCTGATGACACATTTGGCAGTTTAATAGATGTTACTCAA	2488
Db	661	TACAGGCCCTTAAAGCACAGTCTGATGACACATTTGGCAGTTTAATAGATGTTACTCAA	720
Qy	2489	GAATTTTTTAAGAACTGTATTTTATTTTTTAAATGGTGTTTTATTACAAGGGACCTTGAA	2548
Db	721	GAATTTTTTAAGAACTGNATTTTATTTTTTGAATGGTGTTTTATTACAAGGGACCTTG-A	779
Qy	2549	CATGTTTTGTATGTTAAATTCAAAAGTAATGCTTCAATCAGATAGTTCTTTTTTCAAGT	2608

Db 780 CATGTTTTGGATGGTAAATTCAAAAGTAATGCTTTAATCAGATAGTTC-TTTTCACAAGT 838

Qy 2609 TCAATACTGTTTTTTCATGTAAATTTTG 2635

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Db 839 TCAAT-CTGGTTTTTCATGTAAATTTGG 864

RESULT 8

BX109539

LOCUS BX109539 783 bp mRNA linear EST 07-FEB-2003

DEFINITION BX109539 Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone  
IMAGp998G221159 ; IMAGE:487341, mRNA sequence.

ACCESSION BX109539

VERSION BX109539.1 GI:27877774

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 783)

AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,  
Radelof,U., Schneider,D. and Korn,B.

TITLE Human UnigeneSet - RZPD3

JOURNAL Unpublished (2003)

COMMENT Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGp998G221159.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Human UnigeneSet - RZPD3 (RZPDLIB No.972)

[http://www.rzpd.de/CloneCards/cgi-](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972)

[bin/showLib.pl.cgi/response?libNo=972](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972) Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

[www.rzpd.de](http://www.rzpd.de)

This clone is available royalty-free from RZPD;

contact RZPD ([clone@rzpd.de](mailto:clone@rzpd.de)) for further information. Seq primer:

M13r, Primer sequence: TTTACACAGGAAACAGCTATGAC.

FEATURES Location/Qualifiers

source

1. .783

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGp998G221159 ; IMAGE:487341"

/sex="female"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="Soares\_pregnant\_uterus\_NbHPU"

/note="Organ: uterus; Vector: pT7T3-Pac; Site\_1: Not I;  
Site\_2: Eco RI; 1st strand cDNA was primed with a Not I -  
oligo(dT) primer [5'

AACTGGAAGAATTCGCGGCCGCCTTTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library



went through one round of normalization. Library  
constructed by M. Fatima Bonaldo."

ORIGIN

Query Match 18.3%; Score 752.2; DB 13; Length 783;  
Best Local Similarity 98.9%; Pred. No. 2.4e-156;  
Matches 777; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

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Qy      2899 AAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAAAATAATTACCCACA 2958
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Db      1 AAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAAAATAATTACCCACA 60

Qy      2959 AATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTTTTCAGTATGAACCTAACTC 3018
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Db      61 AATGCCACCAG--AACTTACGATTCTTCACCTCTTGGGGTTTTTCAGTATGAACCTAACTC 118

Qy      3019 CCCACCCCAACATCTCCCTCCACATTGTCACCATTTCAAAGGGGCCACAGTGACTTTTG 3078
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Db      119 CCCACCCCAACATCTCCCTCCACATTGTCACCATTTCAAAGGGGCCACAGTGACTTTTG 178

Qy      3079 CTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAAATCTTTTACTAGTGT 3138
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Db      179 CTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAAATCTTTTACTAGTGT 238

Qy      3139 GTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATTTTCTAGACTGTCTC 3198
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Db      239 GTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATTTTCTAGACTGTCTC 298

Qy      3199 TGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTATGTATGGATTTAAT 3258
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Db      299 TGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTATGTATGGATTTAAT 358

Qy      3259 CTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCTGAGCTAAATCTAG 3318
          |||
Db      359 CTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCTGAG-TAAATCTAG 417

Qy      3319 GTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTAGCAACCTTCTGCAT 3378
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Db      418 GTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTAGCAACCTTCTGCAT 477

Qy      3379 TCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCA 3438
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Db      478 TCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCA 537

Qy      3439 GATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGTTTGATAAAGCAGTA 3498
          |||
Db      538 GATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGTTTGATAAAGCAGTA 597

Qy      3499 TTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACTTTGAAGTATTATAT 3558
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Db      598 TTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACTTTGAAGTATTATAT 657

Qy      3559 TGTTCCTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCA 3618
          |||
Db      658 TGTTCCTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCA 717

Qy      3619 GACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTTGTTGGGCCATATTT 3678
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Db      718 GACTTCGCCAGACAGATTGCTGATAATAAATTANGTAAGATAATTTGNTGGGCCATATTT 777
Qy      3679 TAGGAC 3684
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Db      778 TANGAC 783

```

RESULT 9

AK042211

LOCUS AK042211 3150 bp mRNA linear HTC 19-SEP-2003

DEFINITION Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630071G03 product:SIMILAR TO ENDOTHELIN RECEPTOR TYPE A, full insert sequence.

ACCESSION AK042211

VERSION AK042211.1 GI:26088888

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3150)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source	1. .3150 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:A630071G03" /db_xref="MGI:2407243" /db_xref="taxon:10090" /clone="A630071G03" /tissue_type="thymus" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="3 days neonate"
misc_feature	1. .3150 /note="SIMILAR TO ENDOTHELIN RECEPTOR TYPE A (SPTR Q91VV2, evidence: FASTY, 97.7%ID, 72.1%length, match=924)"

ORIGIN

Query Match 18.3%; Score 750.6; DB 11; Length 3150;  
Best Local Similarity 75.5%; Pred. No. 5.7e-156;  
Matches 1029; Conservative 0; Mismatches 289; Indels 45; Gaps 6;

Qy 22 GGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGGAGACGGGGAGGACAGACTGGA 81

Db	9	GGTCCCAGAGTAGAGAGGAAGGTCTAGGAGCCTGTGGAGTCTAAGGAAGATC--GCGGGA	66
Qy	82	GGCGTGTTCCTCCGGAGTTTTCTTTTTCTGTCGAGCCCTCGCGCGCGGTACAGTCATCC	141
Db	67	GGCGTGTTCCTCCGGAGTTTGCTTTTCCTTGGGAGCCTCGCCGCGCACACCCA---TCCC	123
Qy	142	CGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATCCATCCCACCCGGTCGTC	201
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Qy	202	GCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAGTGCCCAGGAAGTTTTCT	261
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Qy	262	GAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGCCGGAGCCCGGGACACCGGCCA	321
Db	230	CTGTCCGGGGAAGTT----TCCCCGAGCTGAGACTGTGCTGCAGCCCTGGTCACCCGCCA	285
Qy	322	CCCTCCGCGCCACCCACCTCGCTTTCTCCGGCTTCTCTGGCCCAGGCGCCGCGCGGAC	381
Db	286	CCCTGCGCGCCACCTCGTTCTCCAGCTCAGGCTCCGGCTGGCCCGTGCGC-----GGA	339
Qy	382	CCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAAAAGTGAAGGTGTAAAAGC	441
Db	340	CCTGGAGCTGTCTGCTTCCGAGGAGCTCTAAGGTGAAAAAAGAAAGGCGTGAGACCAAC	399
Qy	442	AGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAGATGGAACCCCTTTGCCT	501
Db	400	ATAAGAAG-----ACTTAAATCCAGGTTAAGATGAGTATCTTTTGCCT	443
Qy	502	CAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGTGATAATCCTGAGAGATA	561
Db	444	TGCGGCATACTTTTGGCTGACCATGGTGGGAGGCGTAATGGCTGACAATCCGGAGAGATA	503
Qy	562	CAGCACAAATCTAAGCAATCATGTGGATGATTTCCACCTTTTCGTGGCACAGAGCTCAG	621
Db	504	CAGCGCTAATCTAAGCAGCCACATGGAAGACTTCACCCCTTTTCCGGGGACGGAGATCAA	563
Qy	622	CTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCACCCAGCAATGGCTCAATGCA	681
Db	564	CTTTCTGGGCACCACCCATCGACCCCTAATTTGGCCCTGCCTAGCAATGGCTCAATGCA	623
Qy	682	CAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGAT	741
Db	624	CGGCTATTGCCACAGCAGACTAAAATCACGACAGCTTTCAAATATATTAACACTGTGAT	683
Qy	742	ATCTTGTAATTTTTATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTA	801
Db	684	ATCCTGCACCATTTTATCGTGGGAATGGTGGGGAACGCAACTCTACTACGAATCATTTA	743
Qy	802	CCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGA	861
Db	744	CCAAAACAAGTGTATGAGGAACGGCCCCAATGCGCTCATAGCCAGCCTGGCCCTTGGAGA	803
Qy	862	CCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTG	921

Db 804 CCTTATCTACGTGGTCATTGACCTCCCCATCAACGTGTTTAAGCTCTTGGCAGGACGCTG 863

Qy 922 GCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTCAGAA 981  
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Db 864 GCCTTTTCGACCACAATGATTTTGGAGTGTTTCTCTGCAAGCTGTTCCCCTTCCTGCAGAA 923

Qy 982 GTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGC 1041  
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Db 924 GTCCTCCGTGGGCATCACCGTCTTGAACCTCTGTGCTCTCAGTGTGGACAGGTACAGAGC 983

Qy 1042 AGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCTTTGGTAACTGCCATTGAAAT 1101  
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Db 984 AGTGGCTTCCTGGAGCCGAGTTCAAGGAATCGGGATCCCCTTGATTACCGCCATTGAAAT 1043

Qy 1102 TGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCCTGAAGCGATTGGCTTCGTCAT 1161  
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Db 1044 CGTCTCCATCTGGATTCTTTCCTTCATCTTGGCCATCCCGGAAGCAATCGGCTTCGTCAT 1103

Qy 1162 GGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCCACATCAAA 1221  
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Db 1104 GGTACCCTTCGAATACAAGGGCGAGCTGCATAGGACCTGCATGCTCAACGCCACGTCCAA 1163

Qy 1222 ATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTAT 1281  
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Db 1164 GTTCATGGAGTTTTACCAAGATGTGAAGGACTGGTGGCTCTTTGGGTTCTACTTCTGCAT 1223

Qy 1282 GCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAG 1341  
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Db 1224 GCCCTTGGTGTGCACAGCAATCTTCTACACCCTCATGACCTGTGAGATGCTCAACAGGAG 1283

Qy 1342 GAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG 1384  
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Db 1284 GAACGGCAGCTTGC GGATCGCCCTTAGTGAGCACCTCAAACAG 1326

RESULT 10  
 AI936539/c

LOCUS AI936539 781 bp mRNA linear EST 17-DEC-1999

DEFINITION wd29b09.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
 IMAGE:2329529 3' similar to gb:S57498 ENDOTHELIN-1 RECEPTOR  
 PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AI936539

VERSION AI936539.1 GI:5675409

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 781)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

High quality sequence stop: 456.

## Location/Qualifiers

1. .781

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/db xref="taxon:9606"
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/clone="IMAGE:2329529"
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/lab_host="DH10B"
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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with  
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
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Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-c

NCI\_CGAP\_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made

from the same 3 libraries. The pools consisted of

I.M.A.G.E. clones 297480-302087, 682632-687239,

726408-728711, and 729096-731399. Subtraction by Bento

Soares and M. Fatima Bonaldo. "

## Query Match

17.7%; Score 725.6; DB 9; Length 781;

Best Local Similarity 97.1%; Pred. No. 2e-150;

Matches 748; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

Qy 3336 CAACCTGCCTCAGTCCATTTTAACCTGTAGCAACCTTCTGCATTCATAAATCTTGTAATC 3395

| | |    |    | |    | | | | | | | | | |    | | | | | | | | | |    | | | | | | | | | |    | | | | | | | |    | |

Db 773 CAAACAGCTTCAGTCCATTTT-ACCTGTAGCAACCGTCTGCATTCATAATTCTTGTAGTC 715

773 CAAACAGCTTCAGTCCATTTT-ACCTGTAGCAACCGTCTGCATTCATAATTCTTGTAGTC 715

Qy 3396 ATGTTACCATTAACAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAG 3455

| | | |    | | | | | | |    | | | | | | | | | | | | | |    | | | | | | | | | | | | | | |    |

Db 714 ATGTACCCATTACNAATGGGATATAAGAGCAAGCGTGAAAGCAGATGAGCTGTGACTAAG 655

714 ATGTACCCATTACNAATGGGATATAAGAGCAAGCGTGAAAGCAGATGAGCTGTGACTAAG 655

Qy 3456 CAATATAGGGTTTTGTTTGGTTGGTTGGTTTGATAAAGCAGTATTTGGGGTCATATTGTT 3515

|||||

Db 654 CAATATAGGGTTTGGTTTGGTTGGTTGGTTTGATANAGCAGTATTTGGGGTCATATTGTT 595

654 CAATATAGGGTTTGGTTTGGTTGGTTGGTTTGATANAGCAGTATTTGGGGTCATATTGTT 595

Qy 3516 TCCTGTGCTGGAGCAAAGTCATTACACTTTGAAGTATTATATTGTTCTTATCCTCAATT 3575

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Db 594 TCCTGTGCTGGAGCAAAGTCATTACACTTTGGAGTATTATATTGTTCTTATCCTCAATT 535

594 TCCTGTGCTGGAGCAAAAGTCATTACACTTTGGAGTATTATATTGTTCTTATCCTCAATT 535

Qv 3576 CAATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACAGAT 3635

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Db 534 CAATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACAGAT 475

534 CAATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACAGAT 475

Ov 3636 TGCTGATAATAAATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAA 3695

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Db 474 TGCTGATAATAAATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAA 415

474 TGCTGATAATAAATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAA 415

Qv 3696 CATCAGGTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGC 3755

.....

Db 414 CATCAGGTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGC 355

414 CATCAGGTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGC 355

Qy 3756 AGTCAAATCTATTATTCCACTGGCGCATCATATGCAGTGATATATGCCTATAATATAAGC 3815  
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 Db 354 AGTCAAATCTATTATTCCACTGGCGCATCATATGCAGTGATATATGCCTATAATATAAGC 295  
 Qy 3816 CATAGGTTACACCATTTTGTTTAGACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTT 3875  
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 Db 294 CATAGGTTACACCATTTTGTTTAGACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTT 235  
 Qy 3876 CATATGAAAAAATGCATTTTATAAAATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACG 3935  
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 Db 234 CATATGAAAAAATGCATTTTATAAAATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACG 175  
 Qy 3936 TGCATTTTATTTATGGACTGGTAAGTAACTGTGGTTTACTAGCAGGAATATTTCCAATTT 3995  
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 Db 174 TGCATTTTATTTATGGACTGGTAAGTAACTGTGGTTTACTAGCAGGAATATTTCCAATTT 115  
 Qy 3996 CTACCTTTACTACATCTTTTCAACAAGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCC 4055  
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 Db 114 CTACCTTTACTACATCTTTTCAACAAGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCC 55  
 Qy 4056 CTGAGTTGGCAGTGGCCCATAGTGTAAAATAAAAGTTTACAGAAACCTT 4105  
 |||||||||||||||||||||||||||||||||| ||| || |||||  
 Db 54 CTGAGTTGGCAGTGGCCCATAGTGTAAAATAAAAGTTAACAAAACCTT 5

RESULT 11

BM719244

LOCUS BM719244 733 bp mRNA linear EST 01-MAR-2002

DEFINITION UI-E-E01-ajd-b-04-0-UI.r1 UI-E-E01 Homo sapiens cDNA clone  
 UI-E-E01-ajd-b-04-0-UI 5', mRNA sequence.

ACCESSION BM719244

VERSION BM719244.1 GI:19037818

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 733)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics  
 University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa

Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).

Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers

1. .733

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-E-E01-ajd-b-04-0-UI"

/tissue\_type="fetal eye"

/dev\_stage="fetal"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-E-E01"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I;

UI-E-E01 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 17.3%; Score 710.4; DB 12; Length 733;

Best Local Similarity 99.4%; Pred. No. 4.8e-147;

Matches 722; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy      3162 TGTA AATTTCTTTT TAGCCCATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTG 3221
          |||
Db        1 TGTA AATTTCTTTT TAGCCCATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTG 60

Qy      3222 ATATATGCATGTGTGTGATGGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGC 3281
          |||
Db        61 ATATATGCATGTGTGTGATGGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGC 120

Qy      3282 AGTTGTGCCAAAGTGCATAGTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCT 3341
          |||
Db       121 AGTTGTGCCAAAGTGCATAGTCTGAG-TAAAATCTAGGTGATTGTTTCATCATGACAACCT 179

Qy      3342 GCCTCAGTCCATTTTAACTGTAGCAACCTTCTGCATTCAATAATCTTGTAATCATGTTA 3401
          |||
Db       180 GCCTCAGTCCATTTTAACTGTAGCAACCTTCTGCATCCATAAATCTTGTAATCATGTTA 239

Qy      3402 CCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATAT 3461
          |||
Db       240 CCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATAT 299

Qy      3462 AGGGTTTTGTTTGGTTGGTTGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGT 3521
          |||
Db       300 AGGGTTTTGTTTGGTTGGTTGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGT 359
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Qy 3522 GCTGGAGCAAAAGTCATTACACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGT 3581  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 360 GCTGGAGCAAAAGTCATTACACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGT 419  
 Qy 3582 GGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGA 3641  
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 Db 420 GGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGA 479  
 Qy 3642 TAATAAATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAG 3701  
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 Db 480 TAATAAATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAG 539  
 Qy 3702 GTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAA 3761  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 540 GTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAN 599  
 Qy 3762 ATCTATTATTCCACTGGCGCATCATATGCAGTGATATATGCCTATAATATAAGCCATAGG 3821  
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 Db 600 ATCTATTATTCCACTGGCGCATCATATGCAGTGATATATGCCTATAATATAAGCCATAGG 659  
 Qy 3822 TTCACACCATTTTGTTTAGACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATG 3881  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 660 TTCACACCATTTTGTTTAGACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATG 719  
 Qy 3882 AAAAAA 3887  
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 Db 720 NAAAAA 725

RESULT 12

BQ018994/c

LOCUS BQ018994 777 bp mRNA linear EST 27-MAR-2002

DEFINITION UI-H-DH1-awv-o-07-0-UI.s1 NCI\_CGAP\_DH1 Homo sapiens cDNA clone  
 IMAGE:5824350 3', mRNA sequence.

ACCESSION BQ018994

VERSION BQ018994.1 GI:19754271

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 777)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES Location/Qualifiers



```

|||||
Db      390 ACTTCTTTAATTGATCTAATTTACATATTTCTGCGTGTGTATTTCAGCACTAAAAAATGGT 331
Qy      2014 GGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTTTTGC 2073
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Db      330 GGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTTTTGC 271
Qy      2074 ATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAA 2133
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Db      270 ATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAA 211
Qy      2134 TGGGAAC TGGTCACCATGAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTTTAAG 2193
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Db      210 TGGGAAC TGGTCACCATGAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTTTAAG 151
Qy      2194 TGA-TTTTTTGTCTTCAGCCAAACACAATATGGGCTCAGGTCACCTTTTATTTGAAATGT 2252
|||
Db      150 TGATTTTTTTGTCTTCAGCCAAACACAATATGGGCTCAAGTCACCTTTTATTTGAAATGT 91
Qy      2253 CATTTGGTGCCAGTATTTTTTTAACTGCATAATAGCCTAACATGATTATTTGAACTTATTT 2312
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Db      90 CATTTGGTGCCAGTATTTTTTTAACTGCATAATAGCCTAACATGATTATTTGAACTTATTT 31
Qy      2313 ACACATAGTTTGAAAAAAAAAAGACAAAAA 2342
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Db      30 ACACATAGTTTGAAAAAAAAAAGACAAAAA 1

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# RESULT 13

AU139639

LOCUS AU139639 764 bp mRNA linear EST 05-AUG-2002

DEFINITION AU139639 PLACE1 Homo sapiens cDNA clone PLACE1011029 5', mRNA sequence.

ACCESSION AU139639

VERSION AU139639.1 GI:11001160

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 764)

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project

JOURNAL Unpublished (2000)

COMMENT Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES	Location/Qualifiers
source	1. .764 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="PLACE1011029" /tissue_type="placenta" /clone_lib="PLACE1" /note="Vector: pME18SFL3"

Qy	2322	TTGAAAAAAAAAAGACAAAAATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGT	2381
Db	5	TTTGTAAAAAAAAAAGACAAAAATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGT	64
Qy	2382	CACTATTTATTTTTTTTAAACACAAATTCCTAAAGCTACAACAAATACTACAGGCCCTTAA	2441
Db	65	CACTGTTTATTTTTTTTAAACACAAATTCCTAAAGCTACAACAAATACTACAGGCCCTTAA	124
Qy	2442	AGCACAGTCTGATGACACATTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGA	2501
Db	125	AGCACAGTCTGATGACACATTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGA	184
Qy	2502	ACTGTATTTTATTTTTTTAAATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATG	2561
Db	185	ACTGTATTTTATTTTTTTAAATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATG	244
Qy	2562	TTAAATTCAAAGTAATGCTTCAATCAGATAGTTCTTTTTCACAAGTTCAATACTGTTTT	2621
Db	245	TTAAATTCAAAGTAATGCTTCAATCAGATAGTTCTTTTTCACAAGTTCAAT-CTGTTTT	303
Qy	2622	TCATGTAAATTTTGTATGAAAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCAT	2681
Db	304	TCATGTAAATTTTGTATGAAAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCAT	363
Qy	2682	TTAACTCTGCCTGAGACTTTCAGTGCAC'TGTATATAGAAGTCTAAAACACACCTAAGAGA	2741
Db	364	TTAACTCTGCCTGAGACTTTCAGTGCAC'TGTATATAGAAGTCTACAACACACCTAAGAGA	423
Qy	2742	AAAAGATCGAATTTTTTCAGATGATTTCGGAATTTTCATTCAGGTATTTGTAATAGTGACA	2801
Db	424	AAAAGATCGAATTTTTTCAGATGATTTCGGAATTTTCATTCAGGTATTTGTAATAGTGACA	483
Qy	2802	TATATATGTATATACATATCACCTCCTATTCTCTTAATTTTTGTTAAATGTAACTGGC	2861
Db	484	TATATATGTATATACATATCACCTCCTATTCTCTTAATTTTTGTTAAATGTAACTGGC	543
Qy	2862	AGTAAGTCTTTTTTGATCATTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAG	2921
Db	544	AGTAAGTCTTTTTTGATCATTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGNCAG	603
Qy	2922	ATGAGTTTATCATGTCAAGTGAATAAATTACCCACAAATGCCACCAGTAACCTTAACGAT	2981

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Db      604 ATGAGTTTATCATGTCTAGTGAAAAATAATTACCCACAAATGCCACCAG--AACTTACGAT 661
Qy      2982 TCTTCACTTCTTGGGGTTTTTCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCA 3041
      || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      662 TCCTCACTTCTTGGGGTTTTTCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCA 721
Qy      3042 CATTGTCACCATTTCAAAGGGGCC 3065
      ||||| ||||| ||||||| |
Db      722 CATTGGCACCANTTCAAAGGGGNC 745

```

# RESULT 14

CD246193

LOCUS CD246193 782 bp mRNA linear EST 22-MAY-2003

DEFINITION AGENCOURT\_14126996 NIH\_MGC\_145 Homo sapiens cDNA clone

IMAGE:6912753 5', mRNA sequence.

ACCESSION CD246193

VERSION CD246193.1 GI:31006657

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 782)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: GPCR Consortium

cDNA Library Preparation: GPCR Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: IRBI01 row: a column: 08

High quality sequence stop: 640.

## FEATURES

source

Location/Qualifiers

1. .782

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6912753"

/tissue\_type="mixed"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_145"

/note="Vector: pcDNA3.1; Site\_1: varies by clone; Site\_2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',  
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clones represents,  
please visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRBI.preSV.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat)  
a Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 16.9%; Score 694.8; DB 14; Length 782;  
 Best Local Similarity 99.7%; Pred. No. 1.4e-143;  
 Matches 696; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	485	ATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	544
Db	9	ATGGATAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	68
Qy	545	GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTCACCACTTTT	604
Db	69	GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTCACCACTTTT	128
Qy	605	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	664
Db	129	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	188
Qy	665	AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAAA	724
Db	189	AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAAA	248
Qy	725	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGCAACT	784
Db	249	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGCAACT	308
Qy	785	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
Db	309	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	368
Qy	845	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	369	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	428
Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	429	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	488
Qy	965	TTCCCCTTTTTCAGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	489	TTCCCCTTTTTCAGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	548
Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCCTTTG	1084
Db	549	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCCTTTG	608
Qy	1085	GTAAC TGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTTCCTGAA	1144
Db	609	GTAAC TGCCATTGAAATTGTCTCCCTCTGGATCCTGTCCTTTATCCTGGCCATTTCCTGAA	668
Qy	1145	GCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGG	1182
Db	669	GCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGG	706

RESULT 15  
 AI694278/c

LOCUS AI694278 739 bp mRNA linear EST 17-DEC-1999

DEFINITION wd45a01.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
IMAGE:2331048 3' similar to gb:S57498 ENDOTHELIN-1 RECEPTOR  
PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AI694278

VERSION AI694278.1 GI:4971618

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 739)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Insert Length: 1706 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 458.

FEATURES  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2331048"  
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/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NbHL19W, testis NHT, and B-cell  
NCI\_CGAP\_GCB1) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo. "

# ORIGIN

Query Match 16.9%; Score 694.4; DB 9; Length 739;  
Best Local Similarity 98.2%; Pred. No. 1.7e-143;  
Matches 723; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

Qy 3370 CTTCTGCATTCATAAATCTTGTAAATCATGTTACCATACAAATGGGATATAAGAGGCAGC 3429  
||||| ||||||| |||| |||| ||||||| || || |||||||

Db 739 CTTCCGCATTCAT-AATCCTGTATTCATGTT-CCCTTCAAATGGGATATAAGAGGCAGC 682

Qy 3430 GTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGTTTGGAT 3489  
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Db 681 GTGAAAGCAGATGAGCTGTGGACTACAAATATAGGGTTTTGTTTGGTTGGTTGGTTTGGAT 622

Qy 3490 AAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACTTTGAA 3549

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      |||
Db      621 AAAGCAGTATTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACTTGAAA 562

Qy      3550 GTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTCTGATA 3609
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Db      561 GTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTCTGATA 502

Qy      3610 TTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATAATTTGTTGG 3669
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Db      501 TTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATAATTTGTTGG 442

Qy      3670 GCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAGGCTAA 3729
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Db      441 GCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAGGCTAA 382

Qy      3730 GAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATCATATG 3789
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Db      381 GAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATCATATG 322

Qy      3790 CAGTGATATATGCCTATAATATAAGCCATAGGTTTACACCATTTTGTTTAGACAATTGTC 3849
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Db      321 CAGTGATATATGCCTATAATATAAGCCATAGGTTTACACCATTTTGTTTAGACAATTGTC 262

Qy      3850 TTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATTCAGAAA 3909
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Db      261 TTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATTCAGAAA 202

Qy      3910 GTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAACTGTGG 3969
      |||
Db      201 GTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAACTGTGG 142

Qy      3970 TTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTAACTTT 4029
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Db      141 TTTACTAGCAGGACTATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTAACTTT 82

Qy      4030 GTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTAATAATAA 4089
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Db      81 GTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTAATAATAA 22

Qy      4090 AGTTTACAGAAACCTT 4105
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Db      21 AGTTTACAGAAACCTT 6

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GenCore version 5.1.6  
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Listing first 45 summaries

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# SUMMARIES

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4	4105	100.0	4105	6	AX587759	AX587759 Sequence
5	4105	100.0	4105	9	HSET1R	X61950 H.sapiens m
6	4103	100.0	4105	6	BD231376	BD231376 Genes for
7	4103	100.0	4105	9	S57498	S57498 endothelin
8	4101	99.9	4101	9	HUMETN1R	D90348 Homo sapien
9	4079	99.4	4079	6	AR270694	AR270694 Sequence
10	3183.2	77.5	3305	9	S45956	S45956 endothelin
11	2609.6	63.6	2705	9	BC022511	BC022511 Homo sapi
12	2470	60.2	2595	6	BD169895	BD169895 Method fo
13	2470	60.2	2595	9	D11144S8	D11151 Homo sapien
14	2409.2	58.7	164920	9	AC093908	AC093908 Homo sapi
15	2406.6	58.6	67986	9	AY422989	AY422989 Homo sapi
16	2292	55.8	2337	11	G06463	G06463 human STS W
17	1819.6	44.3	1868	9	S63938	S63938 A-type endo
18	1786.6	43.5	3216	4	BTBETREC	X57765 Bovine mRNA
19	1560.2	38.0	1661	9	S67127	S67127 endothelin
20	1359	33.1	1359	9	S81539	S81539 endothelin-
21	1296.8	31.6	1310	9	HUMEDNRA	L06622 Homo sapien
22	1280.8	31.2	1284	6	AX280871	AX280871 Sequence
23	1280.8	31.2	1284	9	AY275462	AY275462 Homo sapi
24	1122	27.3	1374	4	S80652	S80652 endothelin
25	1103.2	26.9	1284	4	AF416703	AF416703 Ovis arie
26	1088.2	26.5	2696	10	BC008277	BC008277 Mus muscu
27	1048.8	25.5	1180	4	AF311974	AF311974 Oryctolag
28	1021	24.9	1021	11	G10643	G10643 human STS C
29	997	24.3	1436	10	RATENDOR	M60786 Rat endothe
30	951	23.2	1160	9	S81542	S81542 endothelin-
31	765.8	18.7	2944	5	AF040634	AF040634 Gallus ga
32	765.8	18.7	2988	5	AF472618	AF472618 Gallus ga
33	695	16.9	1032	9	S81545	S81545 endothelin-

	34	635	15.5	3767	5	BC044316	BC044316 Xenopus l
	35	632.8	15.4	1650	5	XLU06633	U06633 Xenopus lae
	36	624.6	15.2	810	10	AF039892	AF039892 Mus muscu
	37	514	12.5	530	9	MFU20577	U20577 Macaca fasc
	38	492.4	12.0	531	9	D11144S2	D11145 Homo sapien
	39	487.4	11.9	1435	9	S55547S2	S55772 ETA=endothe
c	40	487.4	11.9	66264	2	AC110065	AC110065 Homo sapi
	41	435.6	10.6	3157	5	BC048223	BC048223 Xenopus l
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# ALIGNMENTS

## RESULT 1

AR177879

LOCUS AR177879 4105 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 1 from patent US 6313276.

ACCESSION AR177879

VERSION AR177879.1 GI:17920234

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 4105)

AUTHORS Imura,H., Nakao,K. and Nakanishi,S.

TITLE Human endothelin receptor

JOURNAL Patent: US 6313276-A 1 06-NOV-2001;

FEATURES Location/Qualifiers

source 1. .4105

/organism="unknown"

/mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 4105; DB 6; Length 4105;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	GAATTCGCGGCCCGCTCTTGCGGTCCCAGAGTGGAGTGGAAGGTCTGGAGCTTTGGGAGG	60
Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCGTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240

Qy	241	GCAGTGGCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGGCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
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Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
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Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
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Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140

Db	1081	 TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	 TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
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Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTGCTG	1440
Db	1381	 GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
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Qy	1561	CATGAATTCATGTATAAACCCTAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	 CATGAATTCATGTATAAACCCTAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
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Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
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Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
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Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
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Db	2281	TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
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Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
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## RESULT 2

E07649

LOCUS E07649 4105 bp RNA linear PAT 29-SEP-1997

DEFINITION cDNA encoding endothelin receptor,ETA-receptor.

ACCESSION E07649

VERSION E07649.1 GI:2175784

KEYWORDS JP 1994157595-A/1.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4105)

AUTHORS Imura,H., Nakao,I. and Nakanishi,S.

TITLE HUMAN ENDOTHELIN RECEPTOR

JOURNAL Patent: JP 1994157595-A 1 03-JUN-1994;  
 SHIONOGI & CO LTD

COMMENT OS Homo sapiens (human)

PN JP 1994157595-A/1

PD 03-JUN-1994

PF 12-JUL-1991 JP 1991172828

PI IMURA HIROO, NAKAO ICHIKAZU, NAKANISHI SHIGETADA PC  
 C07K13/00,C12N5/10,C12N15/12,C12P21/02,(C12N5/10,C12R1:91), PC  
 (C12P21/02,  
 PC C12R1:91);



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CC    strandedness: Double;
CC    topology: Linear;
CC    hypothetical: No;
CC    anti-sense: No;
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# ORIGIN

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Best Local Similarity 100.0%;  Pred. No. 0;
Matches 4105;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCCTCCGGCTTCCTC 360
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Db    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCCTCCGGCTTCCTC 360

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Qy	481		CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
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Db	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100

Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTAAA	2400
Db	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTCCGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCCGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940

Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGTCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGTCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840

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Db      3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG 3840

Qy      3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900
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Db      3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900

Qy      3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960
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Db      3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960

Qy      3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020
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Db      3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020

Qy      4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAAGTG 4080
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Db      4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAAGTG 4080

Qy      4081 TAAATAAAAAGTTTACAGAAACCTT 4105
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Db      4081 TAAATAAAAAGTTTACAGAAACCTT 4105

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# RESULT 3

AX548830

LOCUS AX548830 4105 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 115 from Patent WO02061087.

ACCESSION AX548830

VERSION AX548830.1 GI:25813724

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Burmer,G.C., Roush,C.L. and Brown,J.P.

TITLE Antigenic peptides, such as for G protein-coupled receptors  
(GPCRs), antibodies thereto, and systems for identifying such  
antigenic peptides

JOURNAL Patent: WO 02061087-A 115 08-AUG-2002;  
Lifespan Biosciences, Inc. (US)

FEATURES Location/Qualifiers

source 1. .4105  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 4105; DB 6; Length 4105;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60

Db 1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60

Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTCGTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTCGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCGAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCGAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCGAGGCGCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCGAGGCGCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960

Db	901	 TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	 GCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTGGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGAATTGGGATTCC	1080
Db	1021	 TAGTGTGGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	 TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	 TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	 TATGCTCAATGCCACATCAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTCTCTTTGCTG	1440
Db	1381	 GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1501	 CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	 CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	 TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1740
Db	1681	 CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800



Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTACAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTACAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACCTGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACCTGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTACA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTACA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAAGTGTATTTATTTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAAGTGTATTTATTTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTGTATGA	2640

Qy	2641	AAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACGTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCACGTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480

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 Db 3481 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA 3540  
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 Qy 3541 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT 3600  
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 Db 3541 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT 3600  
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 Db 3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG 3840  
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 Db 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960  
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 Qy 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020  
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 Qy 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080  
 |||  
 Db 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080  
 |||  
 Qy 4081 TAAAATAAAAGTTTACAGAAACCTT 4105  
 |||  
 Db 4081 TAAAATAAAAGTTTACAGAAACCTT 4105  
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RESULT 4

AX587759

LOCUS AX587759 4105 bp DNA linear PAT 10-JAN-2003

DEFINITION Sequence 229 from Patent WO0246467.

ACCESSION AX587759

VERSION AX587759.1 GI:28212399

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1

AUTHORS Bertucci,F., Houlgatte,R., Birnbaum,D., Nguyen,C., Viens,P. and

Fert,V.  
 TITLE Gene expression profiling of primary breast carcinomas using arrays  
 of candidate genes  
 JOURNAL Patent: WO 0246467-A 229 13-JUN-2002;  
 Ipsogen (FR)  
 FEATURES Location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 4105; DB 6; Length 4105;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTCGTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTCGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCCCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCCCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600

Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTACAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTACAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAAGTGCATTTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAAGTGCATTTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAATTCATGGAGTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAATTCATGGAGTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG	1440

Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAAC TTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAAC TTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAC TGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAC TGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCAC TTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAC TGCA	2280
Db	2221	ATATGGGCTCAGGTCAC TTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAC TGCA	2280

Qy	2281	TAATAGCCTAACATGATTATTTGAAC TTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAAC TTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCAC TATTATTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCAC TATTATTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATAC TACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATAC TACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTAAAGAACTGTATTTATTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTAAAGAACTGTATTTATTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTCAG	2760
Qy	2761	ATGATTTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAACAATTGTAAATTTCTTTTAGCCC	3180

Db	3121	 AAAATCTTTTACTAGTGTGTGTGTATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	 ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Db	3241	 GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	 GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	 TGTAGCAACCTTCTGCATTCATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	 AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	 TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	 ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Db	3721	 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
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Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020





Db	1	GAATTCGCGGCCCGCCTCTTGCGGTCCCAGAGTGGAGTGGAAAGGTCTGGAGCTTTGGGAGG	60
Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTCGTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTCGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCCCTCAAATTTGCCT	480
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Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
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Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
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Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
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Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
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Qy	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
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Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	1080
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Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1740

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Qy	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTCCACGTCACATTTATTTTTTTAAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTCCACGTCACATTTATTTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640

Db	2581	 TTCAATCAGATAGTTCTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Db	2641	 AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	 TCAGTGCACCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	 ATGATTTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	 CACCTCCTATTCTCTTAATTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	 TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTT	3000
Db	2941	 GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	 TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	 GGCCACACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	 AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	 ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Db	3241	 GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	 GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	 TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480

Db 3421 AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT 3480

Qy 3481 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA 3540  
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Db 3481 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA 3540

Qy 3541 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCATGTGGTGATGAAATTGCCAGGT 3600  
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Db 3541 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCATGTGGTGATGAAATTGCCAGGT 3600

Qy 3601 TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA 3660  
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Db 3601 TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA 3660

Qy 3661 ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG 3720  
 |||

Db 3661 ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG 3720

Qy 3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG 3780  
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Db 3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG 3780

Qy 3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG 3840  
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Db 3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG 3840

Qy 3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900  
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Db 3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900

Qy 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTATGGACTGGTAAG 3960  
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Db 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTATGGACTGGTAAG 3960

Qy 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTCAACA 4020  
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Db 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTCAACA 4020

Qy 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080  
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Db 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080

Qy 4081 TAAAATAAAAGTTTACAGAAACCTT 4105  
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Db 4081 TAAAATAAAAGTTTACAGAAACCTT 4105

# RESULT 6

BD231376

LOCUS BD231376 4105 bp DNA linear PAT 17-JUL-2003

DEFINITION Genes for assessing cardiovascular status and compositions for use thereof.

ACCESSION BD231376

VERSION BD231376.1 GI:33041146

KEYWORDS JP 2002527079-A/140.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4105)  
AUTHORS Norberg,L.T., Andersson,M.K., Lindstrom,P.H.R. and Jonsson,L.  
TITLE Genes for assessing cardiovascular status and compositions for use  
thereof  
JOURNAL Patent: JP 2002527079-A 140 27-AUG-2002;  
PAIROSEAKENSINGU AB

COMMENT OS Homo sapiens (human)  
PN JP 2002527079-A/140  
PD 27-AUG-2002  
PF 13-OCT-1999 JP 2000576056  
PR 14-OCT-1998 US 60/104286,14-OCT-1998 US 60/104302 PI  
LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI  
RUTGER LINDSTROM,  
PI LENA JONSSON  
PC C12Q1/68,C12N15/09//G01N33/53,G01N33/566,C12N15/00 CC Genes  
for assessing cardiovascular status  
and compositions for  
CC use thereof  
FH Key Location/Qualifiers  
FT source 1. .4105  
FT /organism='Homo sapiens (human)'.  
FEATURES Location/Qualifiers  
source 1. .4105  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

# ORIGIN

Query Match 100.0%; Score 4103; DB 6; Length 4105;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	GAATTCGCGGCCGCCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG	60
Db	1	GAATTCGCGGCCGCCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG	60
Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTCGTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTCGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360

Qy	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCCTTTCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCCTTTCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200



Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAANNAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAAC TTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAAC TTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACC CATAGCTCTGTATTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACC CATAGCTCTGTATTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAAGTACCACCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAAGTACCACCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCAC TCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCAC TCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATT CAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATT CAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100

Db	2041	 AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAAACTTTAG	2160
Db	2101	 CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	 AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	 ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAAC TTATTTACACATAGTTTGAAAAAAAAAGACAAA	2340
Db	2281	 TAATAGCCTAACATGATTATTTGAAC TTATTTACACATAGTTTGAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCAC TATTTATTTTTTAAA	2400
Db	2341	 AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCAC TATTTATTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	 ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTATTTTTTAA	2520
Db	2461	 TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Db	2521	 ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTT CATGTAAATTTTGTATGA	2640
Db	2581	 TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTT CATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	 AAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	 TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTCGGAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	 ATGATTCGGAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	 CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940

Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780

Qy	3781	CATCATATGCAGTGATATATGCC	TATAATATAAGCCATAGGTT	CACACCATTTTGT	TTAG	3840
Db	3781	CATCATATGCAGTGATATATGCC	TATAATATAAGCCATAGGTT	CACACCATTTTGT	TTAG	3840
Qy	3841	ACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTT	CATATGAAAAAATGCATTTTATAA			3900
Db	3841	ACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTT	CATATGAAAAAATGCATTTTATAA			3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG				3960
Db	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG				3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA				4020
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# RESULT 7

S57498

LOCUS S57498 4105 bp mRNA linear PRI 29-JAN-2002

DEFINITION endothelin ET-A receptor [human, mRNA, 4105 nt].

ACCESSION S57498

VERSION S57498.1 GI:298319

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4105)

AUTHORS Arai,H., Nakao,K., Hosoda,K., Ogawa,Y., Nakagawa,O., Komatsu,Y. and Imura,H.

TITLE Molecular cloning of human endothelin receptors and their expression in vascular endothelial cells and smooth muscle cells

JOURNAL Jpn. Circ. J. 56 Suppl 5, 1303-1307 (1992)

MEDLINE 93180293

PUBMED 1291713

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 128422] from the original journal article. This sequence comes from Fig. 5.

## FEATURES

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CDS 485..1768  
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# ORIGIN

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Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTCGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
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Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600

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Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
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Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
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Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
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Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAANNAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTCTGCTCTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTCTGCTCTTGCTG	1440

Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAAC	GTGTATAACGAAATGGACAAGAA	1500
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Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTA	AACTTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTA	AACTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTGTGAGCAAGAAATTT	AAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTGTGAGCAAGAAATTT	AAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCT	CGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCT	CGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG		1740
Db	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG		1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAAGTACCACCCTTAGAAGCACTCCTCGGTACT	CCCAT	1800
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Db	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA		1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA		1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA		1980
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Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT		2040
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Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG		2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAC	TGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAC	TGGTCACCATGAACTTTAG	2160
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Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA		2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTA	ACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTA	ACTGCA	2280
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Db	2281	 TAATAGCCTAACATGATTATTTGAAC TTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
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Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
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Db	2461	 TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
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Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
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Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
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Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
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Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
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# RESULT 8

HUMETN1R

LOCUS HUMETN1R 4101 bp mRNA linear PRI 18-DEC-2002

DEFINITION Homo sapiens mRNA for endothelin-1 receptor, complete cds.

ACCESSION D90348

VERSION D90348.1 GI:219649

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4101)

AUTHORS Hosoda,K., Nakao,K., Hiroshi-Arai, Suga,S., Ogawa,Y., Mukoyama,M.,  
 Shirakami,G., Saito,Y., Nakanishi,S. and Imura,H.

TITLE Cloning and expression of human endothelin-1 receptor cDNA

JOURNAL FEBS Lett. 287 (1-2), 23-26 (1991)

MEDLINE 91348221

PUBMED 1652463

COMMENT These data kindly submitted in computer readable form by: Kazuwa  
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FEATURES Location/Qualifiers

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ORIGIN

Query Match 99.9%; Score 4101; DB 9; Length 4101;  
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 Matches 4101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	65	GGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTCGTGCGAGCCCTCGCG	124
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Qy	125	CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC	184
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Qy	245	TGCCCAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA	304
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Db	541	GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCACTTTT	600
Qy	605	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	664
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Qy	665	AGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAA	724
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Qy	725	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACT	784
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Qy	785	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
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Qy	845	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	841	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	900
Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	901	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	960
Qy	965	TTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	961	TTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1020
Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGAATTGGGATTCCCTTTG	1084
Db	1021	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGAATTGGGATTCCCTTTG	1080
Qy	1085	GTAAGTGCCTATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCTTGCCATTCTTGAA	1144
Db	1081	GTAAGTGCCTATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCTTGCCATTCTTGAA	1140
Qy	1145	GCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1204
Db	1141	GCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1200
Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	1201	CTCAATGCCACATCAAAATTCATGGAGTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1260
Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1324
Db	1261	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1320
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAAATGCCCTCAGTGAACATCTTAAGCAG	1384
Db	1321	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAAATGCCCTCAGTGAACATCTTAAGCAG	1380
Qy	1385	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTGGTTC	1444
Db	1381	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTGGTTC	1440
Qy	1445	CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTATAACGAAATGGACAAGAACCGA	1504
Db	1441	CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTATAACGAAATGGACAAGAACCGA	1500
Qy	1505	TGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG	1564
Db	1501	TGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG	1560
Qy	1565	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1624
Db	1561	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1620
Qy	1625	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1684

Db	1621	 CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1680
Qy	1685	AACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1744
Db	1681	 AACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1740
Qy	1745	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAATC	1804
Db	1741	 AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAATC	1800
Qy	1805	CTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1864
Db	1801	 CTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1860
Qy	1865	TTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1924
Db	1861	 TTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1920
Qy	1925	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1984
Db	1921	 TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1980
Qy	1985	GCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2044
Db	1981	 GCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2040
Qy	2045	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2104
Db	2041	 GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2100
Qy	2105	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAGAGAT	2164
Db	2101	 CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAGAGAT	2160
Qy	2165	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2224
Db	2161	 TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2220
Qy	2225	GGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2284
Db	2221	 GGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2280
Qy	2285	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAAAATA	2344
Db	2281	 AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAAAATA	2340
Qy	2345	GTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAACAC	2404
Db	2341	 GTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAACAC	2400
Qy	2405	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2464
Db	2401	 AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2460
Qy	2465	GCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2524

Db	2461	GCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2520
Qy	2525	TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTCA	2584
Db	2521	TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTCA	2580
Qy	2585	ATCAGATAGTTCTTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTGTATGAAAAA	2644
Db	2581	ATCAGATAGTTCTTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTGTATGAAAAA	2640
Qy	2645	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCAG	2704
Db	2641	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCAG	2700
Qy	2705	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2764
Db	2701	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2760
Qy	2765	TTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2824
Db	2761	TTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2820
Qy	2825	TCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2884
Db	2821	TCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2880
Qy	2885	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCACTGAAA	2944
Db	2881	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCACTGAAA	2940
Qy	2945	AATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTTGGGGTTTTTCAG	3004
Db	2941	AATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTTGGGGTTTTTCAG	3000
Qy	3005	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGCC	3064
Db	3001	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGCC	3060
Qy	3065	CACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3124
Db	3061	CACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3120
Qy	3125	TCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATTT	3184
Db	3121	TCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATTT	3180
Qy	3185	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3244
Db	3181	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3240
Qy	3245	TGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCT	3304
Db	3241	TGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCT	3300
Qy	3305	GAGCTAAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3364
Db	3301	GAGCTAAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3360

Qy	3365	GCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTTACAAATGGGATATAAGAG	3424
Db	3361	GCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTTACAAATGGGATATAAGAG	3420
Qy	3425	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3484
Db	3421	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3480
Qy	3485	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3544
Db	3481	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3540
Qy	3545	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3604
Db	3541	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3600
Qy	3605	TGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3664
Db	3601	TGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3660
Qy	3665	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3724
Db	3661	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3720
Qy	3725	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCTACTGGCGCATC	3784
Db	3721	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCTACTGGCGCATC	3780
Qy	3785	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3844
Db	3781	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3840
Qy	3845	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATTC	3904
Db	3841	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATTC	3900
Qy	3905	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3964
Db	3901	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3960
Qy	3965	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA	4024
Db	3961	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA	4020
Qy	4025	ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTAAG	4084
Db	4021	ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTAAG	4080
Qy	4085	ATAAAAGTTTACAGAAACCTT	4105
Db	4081	ATAAAAGTTTACAGAAACCTT	4101

RESULT 9

AR270694

LOCUS

AR270694

4079 bp

DNA

linear

PAT 10-APR-2003

DEFINITION Sequence 1257 from patent US 6500938.  
 ACCESSION AR270694  
 VERSION AR270694.1 GI:29701928  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 4079)  
 AUTHORS Au-Young, J. and Seilhamer, J.J.  
 TITLE Composition for the detection of signaling pathway gene expression  
 JOURNAL Patent: US 6500938-A 1257 31-DEC-2002;  
 FEATURES Location/Qualifiers  
     source 1. .4079  
             /organism="unknown"  
             /mol\_type="genomic DNA"

ORIGIN

Query Match 99.4%; Score 4079; DB 6; Length 4079;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4079; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	5	TCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGGAGAC	64
Db	1	TCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGGAGAC	60
Qy	65	GGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTCGTGCGAGCCCTCGCG	124
Db	61	GGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTCGTGCGAGCCCTCGCG	120
Qy	125	CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC	184
Db	121	CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC	180
Qy	185	CATCCACCCGGTCGTGCGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAG	244
Db	181	CATCCACCCGGTCGTGCGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAG	240
Qy	245	TGCCCAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA	304
Db	241	TGCCCAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA	300
Qy	305	GCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTCTGGC	364
Db	301	GCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTCTGGC	360
Qy	365	CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAA	424
Db	361	CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAA	420
Qy	425	AGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAG	484
Db	421	AGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAG	480
Qy	485	ATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	544
Db	481	ATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	540



Qy	545	GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCACTTTT	604
Db	541	GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCACTTTT	600
Qy	605	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	664
Db	601	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	660
Qy	665	AGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAA	724
Db	661	AGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAA	720
Qy	725	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACT	784
Db	721	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACT	780
Qy	785	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGTGATAGCC	844
Db	781	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGTGATAGCC	840
Qy	845	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	841	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	900
Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	901	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	960
Qy	965	TTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	961	TTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1020
Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCCCTTG	1084
Db	1021	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCCCTTG	1080
Qy	1085	GTAAC TGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCCTGAA	1144
Db	1081	GTAAC TGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCCTGAA	1140
Qy	1145	GCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1204
Db	1141	GCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1200
Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	1201	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1260
Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1324
Db	1261	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1320
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384
Db	1321	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1380
Qy	1385	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTGCTGGTTC	1444

Db	1381	 CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGCTGGTTC	1440
Qy	1445	CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGA	1504
Db	1441	 CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGA	1500
Qy	1505	TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAAC TTGGCAACCATG	1564
Db	1501	 TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAAC TTGGCAACCATG	1560
Qy	1565	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1624
Db	1561	 AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1620
Qy	1625	CAGTCATGCCTCTGCTGCTGCTGTTACCAAGTCCAAAAGTCTGATGACCTCGGTCCCATG	1684
Db	1621	 CAGTCATGCCTCTGCTGCTGCTGTTACCAAGTCCAAAAGTCTGATGACCTCGGTCCCATG	1680
Qy	1685	AACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCGGAGC	1744
Db	1681	 AACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCGGAGC	1740
Qy	1745	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAATC	1804
Db	1741	 AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAATC	1800
Qy	1805	CTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1864
Db	1801	 CTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1860
Qy	1865	TTCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1924
Db	1861	 TTCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1920
Qy	1925	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1984
Db	1921	 TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1980
Qy	1985	GCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2044
Db	1981	 GCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2040
Qy	2045	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2104
Db	2041	 GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2100
Qy	2105	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGAT	2164
Db	2101	 CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGAT	2160
Qy	2165	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2224
Db	2161	 TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2220
Qy	2225	GGGCTCAGGTCAC TTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTGCATAAT	2284

Db	2221	GGGCTCAGGTCAC TTTTATTTGAAATGTCATTTGGTGCCAGTATTTTAACTGCATAAT	2280
Qy	2285	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAATA	2344
Db	2281	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAATA	2340
Qy	2345	GTATTCAGGTGAGCAATTAGATTAGTATTTCCACGTCAC TATTTATTTTAAACAC	2404
Db	2341	GTATTCAGGTGAGCAATTAGATTAGTATTTCCACGTCAC TATTTATTTTAAACAC	2400
Qy	2405	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2464
Db	2401	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2460
Qy	2465	GCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTAAATGG	2524
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Qy	2525	TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTCA	2584
Db	2521	TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTCA	2580
Qy	2585	ATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2644
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Qy	2645	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCA TTTAACTCTGCCTGAGACTTTCAG	2704
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Qy	2705	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2764
Db	2701	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2760
Qy	2765	TTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2824
Db	2761	TTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2820
Qy	2825	TCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	2884
Db	2821	TCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	2880
Qy	2885	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2944
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Qy	2945	AATAATTACCCACAAATGCCACCAGTAAC TTAACGATTCTTCACTTCTTGGGGTTTTTCAG	3004
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Qy	3185	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3244
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Db	3241	TGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCT	3300
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Db	3301	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3360
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Db	3361	GCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3420
Qy	3425	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3484
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Qy	3545	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3604
Db	3541	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3600
Qy	3605	TGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3664
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Qy	3665	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3724
Db	3661	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3720
Qy	3725	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCGCATC	3784
Db	3721	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCGCATC	3780
Qy	3785	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3844
Db	3781	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3840
Qy	3845	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATTC	3904
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Qy	3905	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3964
Db	3901	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3960

Qy 3965 TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA 4024  
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 Db 3961 TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA 4020  
 Qy 4025 ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA 4083  
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RESULT 10

S45956

LOCUS S45956 3305 bp mRNA linear PRI 08-MAY-1993

DEFINITION endothelin receptor subtype A [human, placenta, mRNA, 3305 nt].

ACCESSION S45956

VERSION S45956.1 GI:257375

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3305)

AUTHORS Hayzer,D.J., Rose,P.M., Lynch,J.S., Webb,M.L., Kienzle,B.K.,  
 Liu,E.C., Bogosian,E.A., Brinson,E. and Runge,M.S.

TITLE Cloning and expression of a human endothelin receptor: subtype A

JOURNAL Am. J. Med. Sci. 304 (4), 231-238 (1992)

MEDLINE 93035452

PUBMED 1415318

REMARK GenBank staff at the National Library of Medicine created this  
 entry [NCBI gibbsq 115436] from the original journal article.  
 This sequence comes from Fig. 2.

FEATURES

source

Location/Qualifiers

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/mol\_type="mRNA"

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ORIGIN

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Best Local Similarity 98.9%; Pred. No. 0;

Matches 3275; Conservative 0; Mismatches 27; Indels 8; Gaps 7;

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Qy	383	CGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAAAAGTGAAGGTGTAAAAGCA	442
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Qy	443	GCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAGATGGAAACCTTTGCCTC	502
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Qy	683	AACTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATA	742
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Qy	803	CAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGAC	862
Db	540	CAGAACAAATATATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGAC	599
Qy	863	CTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGG	922
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Qy	923	CCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTGCAGAAG	982
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Qy	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
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Qy	1343	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Db	1080	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1139
Qy	1403	ACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT	1462
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Qy	1463	ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1200	ATATTGAAGAAAACCTGTGTATAACGAGATGGACAAGAACCGATGTGAATTACTTAGTTTC	1259
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Db	1260	TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC	1319
Qy	1583	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC	1642
Db	1320	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC	1379
Qy	1643	TGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCATGAACGGAACAAGCATCCAG	1702
Db	1380	TGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCATGAACGGAACAAGCATCCAG	1439
Qy	1703	TGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGCATG	1762
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Qy	1763	AACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATATCCTCTCGGAGAAAAAATC	1822
Db	1500	AACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATATCCTCTCGGAGAAAAAATC	1559
Qy	1823	ACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCACTCCCA	1882
Db	1560	ACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCACTCCCA	1619
Qy	1883	CACCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAGACTGGTTTATCCACCCACAACA	1941
Db	1620	CACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGGTAGACTGGTTTATCCACCCACAACA	1679
Qy	1942	TCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTGTATTTCAGCA	2001

Db	1680	 TCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTTCAGCA	1739
Qy	2002	CTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATT	2061
Db	1740	 CTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATT	1799
Qy	2062	TACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTG	2121
Db	1800	 TACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTCCTG	1859
Qy	2122	GTGAATGTTCAATGGGAAGTGGTCACCATGAACTTTAGAGATTAACGACAAGATTTTCT	2181
Db	1860	 GTGAATGTTCACTGGGAAGTGGTCACCATGAACTTTAGAGATTAACGACAAGATTTTCT	1919
Qy	2182	ACTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACACAATATGGGCTCAGGTCACCTT	2240
Db	1920	 ACTTTTTTTAAGTGATTTTTTTGGCCTTCAGCCAAACACAATATGGGCTCAAGTCACCTT	1979
Qy	2241	TATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGATTAT	2300
Db	1980	 TATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGATTAT	2039
Qy	2301	TTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAAAATAGTATTCAGGTGAGCAA	2360
Db	2040	 TTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAAAATAGTATTCAGGTGAGCAA	2099
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Db	2100	 TTAGATTAGTATTTTCCACGTCACATTTATTTTTTTAAACACAAATTCTAAAGCTACA	2159
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Db	2340	 TCACAAGTTCAAT-CTGTTTTTCATGTAAATTTTCGTATGAAAAATCAATGTCAAGTACCA	2398
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Db	2638	ACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTTCAGTGAAAAATAATTACCCACAAA	2697
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Qy	3381	ATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCAGA	3440
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Qy	3441	TGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGTTTGATAAAGCAGTATT	3500
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RESULT 11  
BC022511

LOCUS BC022511 2705 bp mRNA linear PRI 04-OCT-2003  
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 VERSION BC022511.1 GI:18490297  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2705)  
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 MEDLINE 22388257  
 PUBMED 12477932  
 REFERENCE 2 (bases 1 to 2705)  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 32 Row: j Column: 7  
This clone was selected for full length sequencing because it  
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ORIGIN

Query Match                      63.6%;    Score 2609.6;    DB 9;    Length 2705;  
Best Local Similarity    99.3%;    Pred. No. 0;  
Matches 2673;    Conservative    0;    Mismatches    14;    Indels        5;    Gaps        5;

Qy	134	AGTCATCCC	GCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATCCATCCCACC	193
Db	1	AGTCATCCC	GCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATCCATCCCACC	60
Qy	194	CGGTCGTCG	CGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAGTGCCCGAGGA	253
Db	61	CGGTCGTCG	CGCGGGGATTGGGGTCCCAGCGAGACCTCCCCGGGAGAAGCAGTGCCCGAGGA	120
Qy	254	AGTTTTCTG	AAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGCGGAGCCCGGGAC	313
Db	121	AGTTTTCTG	AAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGCGGAGCCCGGGAC	180
Qy	314	ACCGGCCAC	CCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTCTGGCCCAGGCGCC	373
Db	181	ACCGGCCAC	CCTCCGCGCCACCCACCCTCGCCGGCTCCGGCTTCCTCTGGCCCAGGCGCC	240

Qy	374	GCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAAAAGTGAAGGT	433
Db	241	GCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTG-AAAAAAAAAGTGAAGGT	299
Qy	434	GTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCCCTCAAATTTGCCTCAAGATGGAAACC	493
Db	300	GTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCCCTCAAATTTGCCTCAAGATGGAAACC	359
Qy	494	CTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGTGATAATCCT	553
Db	360	CTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGTGATAATCCT	419
Qy	554	GAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACACTTTTCGTGGCACA	613
Db	420	GAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACACTTTTCGTGGCACA	479
Qy	614	GAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCCAGCAATGGC	673
Db	480	GAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCCAGCAATGGC	539
Qy	674	TCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAAAC	733
Db	540	TCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAAAC	599
Qy	734	ACTGTGATATCTTGTAATATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGG	793
Db	600	ACTGTGATATCTTGTAATATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGG	659
Qy	794	ATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCC	853
Db	660	ATCATTTACCAGAACAAATGTATGAGGAATGGCCACAACGCGCTGATAGCCAGTCTTGCC	719
Qy	854	CTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCT	913
Db	720	CTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCT	779
Qy	914	GGGCGCTGGCCTTTTGATCACAAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTT	973
Db	780	GGGCGCTGGCCTTTTGATCACAAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTT	839
Qy	974	TTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGG	1033
Db	840	TTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGG	899
Qy	1034	TACAGAGCAGTTGCCCTCCTGGAGTCGTGTTTACAGGAATTGGGATTCCTTTGGTAACCTGCC	1093
Db	900	TACAGAGCAGTTGCCCTCCTGGAGTCGTGTTTACAGGAATTGGGATTCCTTTGGTAACCTGCC	959
Qy	1094	ATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGC	1153
Db	960	ATTGAAATTGTCTCCATCTGGATCCTGTCGTTTATCCTGGCCATTCTGAAGCGATTGGC	1019
Qy	1154	TTCGTCATGGTACCCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC	1213
Db	1020	TTCGTCATGGTACCCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC	1079

Qy	1214	ACATCAAAATTCATGGAGTTCACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTCTAT	1273
Db	1080	ACATCAAAATTCATGGAGTTCACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTCTAT	1139
Qy	1274	TTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTG	1333
Db	1140	TTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTG	1199
Qy	1334	AACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAA	1393
Db	1200	AACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAA	1259
Qy	1394	GTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTCCCTCTTCAC	1453
Db	1260	GTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTCCCTGTTCAT	1319
Qy	1454	TTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGATGTGAATTA	1513
Db	1320	TTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAGATGGACAAGAACCGATGTGAATTA	1379
Qy	1514	CTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAAC TTGGCAACCATGAATTCATGT	1573
Db	1380	CTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAAC TTGGCAACCATGAATTCATGT	1439
Qy	1574	ATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGC	1633
Db	1440	ATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGC	1499
Qy	1634	CTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCATGAACGGAACA	1693
Db	1500	CTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCATGAACGGAACA	1559
Qy	1694	AGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGCAGCCATAAG	1753
Db	1560	AGCATCCAGTGGAAGGACCACGATCAAAACAACCACAACACAGACCGGAGCAGCCATAAG	1619
Qy	1754	GACAGCATGAAGTACCACCTTAGAAGCACTCCTCGGTACTCCCATAATCCTCTCGGAG	1813
Db	1620	GACAGCATGAAGTACCACCTTAGAAGCACTCCTCGGTACTCCCATAATCCTCTCGGAG	1679
Qy	1814	AAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTCTTCCTTAAT	1873
Db	1680	AAAAAAATCACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATCCTTCTTCCTTAAT	1739
Qy	1874	TCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAGACTGGTTTATCCA	1932
Db	1740	TCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGGTAGACTGGTTTATCCA	1799
Qy	1933	CCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTG	1992
Db	1800	CCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTG	1859
Qy	1993	TATTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAG	2052
Db	1860	TATTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAG	1919
Qy	2053	AAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATG	2112

Db	1920	 AAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGGCTAGCTTTTATG	1979
Qy	2113	GCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGATTAACGACA	2172
Db	1980	 GCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGATTAACGACA	2039
Qy	2173	AGATTTTCTACTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACACAATATGGGCTCA	2231
Db	2040	 AGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATATGGGCTCA	2099
Qy	2232	GGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAATAGCCTAA	2291
Db	2100	 AGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAATAGCCTAA	2159
Qy	2292	CATGATTATTTGAACTTATTTACACATAGTTTG-AAAAAAAAAAGACAAAAATAGTATTC	2350
Db	2160	 CATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAATAGTATTC	2219
Qy	2351	AGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAAACACAAATTC	2410
Db	2220	 AGGTGAGCAATTAGATTAGTATTTTCCACGTCAGTGTATTTTTTAAACACAAATTC	2279
Qy	2411	TAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTGGCAGTT	2470
Db	2280	 TAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTGGCAGTT	2339
Qy	2471	TAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGGTGTTTT	2530
Db	2340	 TAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGGTGTTTT	2399
Qy	2531	ATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTCAATCAGA	2590
Db	2400	 ATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTCAATCAGA	2459
Qy	2591	TAGTTCCTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAAATCAATG	2650
Db	2460	 TAGTTCCTTTTTCACAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAAATCAATG	2518
Qy	2651	TCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCAGTGCAC	2710
Db	2519	 TCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCAGTGCAC	2578
Qy	2711	GTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGATTCGGA	2770
Db	2579	 GTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGATTCAGA	2638
Qy	2771	AATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCA	2822
Db	2639	 AATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCA	2690

RESULT 12

BD169895

LOCUS BD169895 2595 bp DNA linear PAT 17-JAN-2003

DEFINITION Method for examination of allergosis.

ACCESSION BD169895

VERSION BD169895.1 GI:27875707  
 KEYWORDS WO 02052006-A/28.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2595)  
 AUTHORS Otani,N., Matsui,K., Yoshida,N., Sugita,Y. and Izuhara,K.  
 TITLE Method for examination of allergosis  
 JOURNAL Patent: WO 02052006-A 28 04-JUL-2002;  
 GENOX RESEARCH INC,NORIKO OTANI,KEIKO MATSUI,NEI YOSHIDA, YUJI  
 SUGITA, KENJI IZUHARA  
 COMMENT OS Homo sapiens (human)  
 PN WO 02052006-A/28  
 PD 04-JUL-2002  
 PF 21-DEC-2001 WO 2001JP011287  
 PR 26-DEC-2000 JP 00P 396166  
 PI NORIKO OTANI,KEIKO MATSUI,NEI YOSHIDA,YUJI SUGITA,KENJI PI  
 IZUHARA  
 PC C12N15/12,C12Q1/68,C12Q1/02,A01K67/027,A61K31/713,A61K45/00,  
 PC A61K48/00,  
 PC A61P37/08,G01N33/15,G01N33/50,G01N33/53  
 CC Method for examination of allergosis  
 FH Key Location/Qualifiers  
 FT source 1. .2595  
 FT /organism='Homo sapiens (human)'.  
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 source 1. .2595  
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 Query Match 60.2%; Score 2470; DB 6; Length 2595;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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 Db 15 CCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCAT 74  
 Qy 1684 GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCGGAG 1743  
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 Db 75 GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCGGAG 134  
 Qy 1744 CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT 1803  
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 Db 135 CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT 194  
 Qy 1804 CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT 1863  
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 Db 195 CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT 254  
 Qy 1864 CTTCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG 1923  
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 Db 255 CTTCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG 314

Qy	1924	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	1983
Db	315	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	374
Qy	1984	TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA	2043
Db	375	TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA	434
Qy	2044	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTA	2103
Db	435	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTA	494
Qy	2104	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAGAGA	2163
Db	495	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAGAGA	554
Qy	2164	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2223
Db	555	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614
Qy	2224	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	2283
Db	615	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	2343
Db	675	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCCTATTTATTTTTTTAAACA	2403
Db	735	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCCTATTTATTTTTTTAAACA	794
Qy	2404	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	GGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	2583
Db	915	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTACAAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	AATCAGATAGTTCTTTTTTACAAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	2763
Db	1094	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	1153
Qy	2764	ATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823



Db	1154	 ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTGTTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	2883
Db	1214	CTCCTATTCTCTTAATTTTTGTTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	2943
Db	1274	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	3063
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCAT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCAT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
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Qy	3364	AGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	AGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	3483
Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	3543
Db	1874	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	3663

Db 1994 CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAAATT 2053  
 Qy 3664 TGT TGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA 3723  
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 Db 2054 TGT TGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA 2113  
 Qy 3724 GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCGCAT 3783  
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 Db 2114 GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCGCAT 2173  
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 Db 2294 CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA 2353  
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 Db 2354 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 2413  
 Qy 4024 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTA 4083  
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 Db 2414 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTA 2473  
 Qy 4084 AATAAAAGTTTACAGAAACCTT 4105  
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 Db 2474 AATAAAAGTTTACAGAAACCTT 2495

RESULT 13

D11144S8

LOCUS D11144S8 2595 bp DNA linear PRI 19-SEP-2002

DEFINITION Homo sapiens gene for endothelin-A receptor, complete cds, exon 8 and 3' flanking region.

ACCESSION D11151

VERSION D11151.1 GI:219628

KEYWORDS G protein-coupled receptor; endothelium; smooth muscle.

SEGMENT 8 of 8

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2595)

AUTHORS Hosoda,K., Nakao,K., Tamura,N., Arai,H., Ogawa,Y., Suga,S., Nakanishi,S. and Imura,H.

TITLE Organization, structure, chromosomal assignment, and expression of the gene encoding the human endothelin-A receptor

JOURNAL J. Biol. Chem. 267 (26), 18797-18804 (1992)

MEDLINE 92406798

PUBMED 1326535

REFERENCE 2 (bases 1 to 2595)

AUTHORS Hosoda, K.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-MAY-1992) Kiminori Hosoda, Kyoto University School of  
 Medicine, Department of Medicine; 54 Shogoin Kawahara-cho,  
 Sakyo-ku, Kyoto, Kyoto 606, Japan (Tel:81-75-751-3170,  
 Fax:81-75-771-9452)

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# RESULT 14

AC093908

LOCUS AC093908 164920 bp DNA linear PRI 01-MAR-2002

DEFINITION Homo sapiens BAC clone RP11-752L20 from 4, complete sequence.

ACCESSION AC093908 AC067873

VERSION AC093908.3 GI:18497272

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 164920)

AUTHORS Sulston, J.E. and Waterston, R.

TITLE Toward a complete human genome sequence

JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

MEDLINE 99063792

PUBMED 9847074

REFERENCE 2 (bases 1 to 164920)

AUTHORS Paulson, E., Cotton, M. and Creason, K.

TITLE The sequence of Homo sapiens BAC clone RP11-752L20

JOURNAL Unpublished (2001)  
 REFERENCE 3 (bases 1 to 164920)  
 AUTHORS Waterston,R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-SEP-2001) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 REFERENCE 4 (bases 1 to 164920)  
 AUTHORS Waterston,R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-FEB-2002) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 REFERENCE 5 (bases 1 to 164920)  
 AUTHORS Waterston,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-FEB-2002) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 REFERENCE 6 (bases 1 to 164920)  
 AUTHORS Waterston,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 COMMENT On Feb 5, 2002 this sequence version replaced gi:15778805.  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu/gsc>  
 Contact: [sapiens@watson.wustl.edu](mailto:sapiens@watson.wustl.edu)  
 ----- Summary Statistics  
 Center project name: H\_NH0752L20  
 Drafting Center: WIBR  
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NOTICE: This sequence may not represent the entire insert of this  
 clone. It may be shorter because we only sequence overlapping  
 clone sections once, or longer because we provide a small overlap  
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate  
 chemistry, or covered by high quality data (i.e., phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by sequence  
 from more than one subclone; and the assembly was confirmed by  
 restriction digest.

#### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D.  
 McPherson, Department of Genetics, Washington University, St. Louis  
 MO. For additional information about the map position of this  
 sequence, see <http://genome.wustl.edu/gsc>

#### SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male  
 donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,  
 Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved

approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>  
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-56F3. Actual start of this clone is at base position 1 of RP11-752L20; actual end is at base position 164920 of RP11-752L20.

Data from AC083898 was used to finish this clone, AC093908.

The sequence of AC067873 has been incorporated into AC093908.

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RESULT 15

AY422989

LOCUS AY422989 67986 bp DNA linear PRI 04-OCT-2003

DEFINITION Homo sapiens endothelin receptor type A (EDNRA) gene, complete cds.

ACCESSION AY422989

VERSION AY422989.1 GI:36968339

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 67986)

AUTHORS Rieder,M.J., Livingston,R.J., Daniels,M.R., Montoya,M.A.,  
 Chung,M.-W., Miyamoto,K.E., Nguyen,C.P., Nguyen,D.A., Poel,C.L.,  
 Robertson,P.D., Schackwitz,W.S., Sherwood,J.K., Witrak,L.A. and  
 Nickerson,D.A.

TITLE Direct Submission

JOURNAL Submitted (25-SEP-2003) Genome Sciences, University of Washington,  
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 Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA  
 (URL: <http://egp.gs.washington.edu>).

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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13	1819.6	44.3	1868	3	AAF20903	Aaf20903	Human low
14	1819.6	44.3	1868	7	ABZ96609	Abz96609	Human end
15	1819.6	44.3	1868	7	ABZ96597	Abz96597	Human end
16	1819.6	44.3	2008	3	AAA34782	Aaa34782	Human ade
17	1819.6	44.3	2008	3	AAF20904	Aaf20904	Human low
18	1819.6	44.3	2008	7	ABZ96598	Abz96598	Human nuc
19	1819.6	44.3	5036	3	AAF21447	Aaf21447	Human end
20	1819.6	44.3	5036	7	ABZ97141	Abz97141	Human end
21	1819.6	44.3	117608	7	ABZ97129	Abz97129	Human rec
22	1819.6	44.3	117609	3	AAF21435	Aaf21435	Human rec
23	1296.8	31.6	1310	3	AAA34780	Aaa34780	Human ade
24	1296.8	31.6	1310	3	AAA34792	Aaa34792	Human ade
25	1296.8	31.6	1310	3	AAF20902	Aaf20902	Human end
26	1296.8	31.6	1310	3	AAF20914	Aaf20914	Human ELA
27	1296.8	31.6	1310	7	ABZ96608	Abz96608	Human ELA
28	1296.8	31.6	1310	7	ABZ96596	Abz96596	Human nuc
29	1296.8	31.6	146981	3	AAF21442	Aaf21442	Human ELA
30	1296.8	31.6	146982	7	ABZ97136	Abz97136	Human ELA
31	1280.8	31.2	1284	5	ABI97987	Abi97987	Non-endog
32	1266.8	30.9	1300	7	ABZ97244	Abz97244	Human end
33	1248.8	30.4	1284	2	AAQ63209	Aaq63209	Human end
34	521	12.7	560	6	ABZ34947	Abz34947	Human gen
35	412.4	10.0	451	8	ACH21748	Ach21748	Human adu
36	403.8	9.8	1965	2	AAQ25892	Aaq25892	Sequence
37	403.8	9.8	2018	9	ADB52872	Adb52872	Primary r
38	399	9.7	4301	2	AAQ34584	Aaq34584	ETb recep
39	396.6	9.7	1406	2	AAQ53922	Aaq53922	Bovine ET
40	395.8	9.6	1470	7	ACA56605	Aca56605	Human sig
41	395.8	9.6	1632	6	AAD24966	Aad24966	Human G-p
42	395.8	9.6	1719	3	AAF21285	Aaf21285	Human low
43	395.8	9.6	1719	7	ABZ96979	Abz96979	Human nuc
44	395.8	9.6	1720	3	AAA35163	Aaa35163	Human ade
45	395.8	9.6	1872	3	AAA35161	Aaa35161	Human ade

# ALIGNMENTS

## RESULT 1

ABZ35259

ID ABZ35259 standard; cDNA; 4105 BP.

XX

AC ABZ35259;

XX

DT 05-FEB-2003 (first entry)

XX

DE Human gene expression profile polynucleotide SEQ ID NO 370.

XX

KW Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;

KW bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;

KW tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;

KW gene expression; gene; ss.

XX  
 OS Homo sapiens.  
 XX  
 PN WO200274979-A2.  
 XX  
 PD 26-SEP-2002.  
 XX  
 PF 20-MAR-2002; 2002WO-US008456.  
 XX  
 PR 20-MAR-2001; 2001US-0276947P.  
 XX  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 XX  
 PI Wan J, Wang Y;  
 XX  
 DR WPI; 2002-740862/80.  
 XX  
 PT New gene expression profile generated from primary, endothelial,  
 PT epithelial, and muscle cell types, useful for identifying disease  
 PT pathologies involving alterations of gene expression, e.g. cancer.  
 XX  
 PS Disclosure; Page 513-515; 850pp; English.  
 XX  
 CC The invention relates to a gene expression profile comprising one or more  
 CC genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type  
 CC is a coronary artery endothelium, umbilical artery or vein endothelium,  
 CC aortic endothelium, dermal microvascular endothelium, pulmonary artery  
 CC endothelium, myometrium microvascular endothelium, keratinocyte  
 CC epithelium, bronchial epithelium, mammary epithelium, prostate  
 CC epithelium, renal cortical epithelium, renal proximal tubule epithelium,  
 CC small airway epithelium, renal epithelium, umbilical artery smooth  
 CC muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,  
 CC dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,  
 CC aortic smooth muscle, mesangial cells, coronary artery smooth muscle,  
 CC bronchial smooth muscle, uterine smooth muscle, lung fibroblast,  
 CC osteoblasts or prostate stromal cell. The gene expression profile is used  
 CC for determining the level of RNA expression for a sample, determining the  
 CC phenotype of a cell and distinguishing cell types. The gene or a protein  
 CC expression profile is useful in identifying disease pathologies involving  
 CC alterations of gene expression. The assessment of expression profiles may  
 CC provide meaningful information with respect to tumour type and stage,  
 CC treatment methods, and prognosis. The gene or protein expression profile  
 CC may also be used for creating microarrays. The microarray is useful for  
 CC genetic and physical mapping of genomes, DNA sequencing, genetic or  
 CC medical diagnosis, genotyping of organisms, confirming cell or tissue  
 CC identifications and in identifying promising antibiotics, antiviral or  
 CC antifungal agents  
 XX  
 SQ Sequence 4105 BP; 1138 A; 859 C; 845 G; 1263 T; 0 U; 0 Other;

Query Match 100.0%; Score 4105; DB 6; Length 4105;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTCTTTTTCTGTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTCTTTTTCTGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATAATTCCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATAATTCCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900

Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800



Db	1741	 GAGCAGCCATAAGGACAGCATGAAC TGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	 AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCAC TCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	 CTTCTTCCTTAATTCAC TCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	 CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATT CAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	 TTCTGCGTGTTGTATT CAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	 AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAC TGGTCACCATGAACTTTAG	2160
Db	2101	 CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAC TGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	 AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	 ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAAC TTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	 TAATAGCCTAACATGATTATTTGAAC TTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCAC TATTTATTTTTTAAA	2400
Db	2341	 AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCAC TATTTATTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	 ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	 TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	 ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640

Db	2581	TTCAATCAGATAGTTCTTTTTTCAACAAGTTCAATACTGTTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCATTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCATTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480

Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Qy	4081	TAAAATAAAAAGTTTACAGAAACCTT	4105
Db	4081	TAAAATAAAAAGTTTACAGAAACCTT	4105

# RESULT 2

ABV94238

ID ABV94238 standard; cDNA; 4105 BP.

XX

AC ABV94238;

XX

DT 08-JAN-2003 (first entry)

XX

DE Breast carcinoma related nucleotide sequence SEQ ID NO:229.

XX

KW Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;

KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200246467-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 07-DEC-2001; 2001WO-IB002811.  
 XX  
 PR 08-DEC-2000; 2000US-0254090P.  
 PR 07-DEC-2001; 2001US-00007926.  
 XX  
 PA (IPSO-) IPSOGEN.  
 XX  
 PI Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;  
 XX  
 DR WPI; 2002-619023/66.  
 XX  
 PT Novel polynucleotide library useful in molecular characterization of a  
 PT carcinoma, comprising a pool of polynucleotide sequences or its  
 PT subsequences which are either underexpressed or overexpressed in tumor  
 PT cells.  
 XX  
 PS Claim 1; Page 258-259; 401pp; English.  
 XX  
 CC The present invention describes a polynucleotide library (I) useful in  
 CC the molecular characterisation of a carcinoma, comprising a pool of  
 CC polynucleotides or its subsequences which are either underexpressed or  
 CC overexpressed in tumour cells, and correspond to any of the  
 CC polynucleotide sequences chosen from the 468 sequences given in ABV94010  
 CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for  
 CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting  
 CC (M1) differentially expressed polynucleotide sequences which are  
 CC correlated with a cancer, involves obtaining a polynucleotide sample from  
 CC a patient, and reacting the polynucleotide sample obtained with a probe  
 CC immobilised on a solid support, where the probe comprises any combination  
 CC of the polynucleotide sequences of (I) or its expression products encoded  
 CC by polynucleotide sequences of (I), and detecting the reaction product.  
 CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)  
 CC is useful in molecular characterisation of a carcinoma. (I) and (II) are  
 CC useful for the prognosis or diagnostic of tumour, in differentiating a  
 CC normal cell from a cancer cell, detecting a hormone sensitive tumour  
 CC cell, differentiating a tumour with lymph nodes from a tumour without  
 CC lymph nodes, differentiating antracycline-sensitive tumours from  
 CC antracycline-insensitive tumours, and classifying good and poor prognosis  
 CC primary breast tumours. (I) is useful for large-scale molecular  
 CC characterisation of breast cancer that help in prediction, prognosis and  
 CC cancer treatment, and for detecting differentially expressed genes that  
 CC correlated with a cancer  
 XX  
 SQ Sequence 4105 BP; 1138 A; 859 C; 845 G; 1263 T; 0 U; 0 Other;

Query Match 100.0%; Score 4105; DB 6; Length 4105;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAATTCGCGGCCGCCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG	60
Db	1	GAATTCGCGGCCGCCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG	60
Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTCTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTCTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGCCACCCTCCGCGCCACCCACCCTCGCTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGCCACCCTCCGCGCCACCCACCCTCGCTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTCCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTCCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCTGCGGACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCTGCGGACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900

Db	841	 AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	 TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	 GCTGTTCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGGAATTGGGATTCC	1080
Db	1021	 TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	 TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Db	1141	 TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	 TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGAC	1320
Db	1261	 CTTCGGGTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGCTG	1440
Db	1381	 GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAACTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAACTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1501	 CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	 CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	 TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740

Db	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTCACTACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTCACTACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTACA	2280
Db	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTACA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAAGTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAAGTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580

Qy	2581	TTCAATCAGATAGTTCTTTTTTCAACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTCAACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCACCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAACTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAACTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420



Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Qy	4081	TAAAATAAAAGTTTACAGAAACCTT	4105
Db	4081	TAAAATAAAAGTTTACAGAAACCTT	4105

RESULT 3

ABZ42662

ID ABZ42662 standard; DNA; 4105 BP.

XX

AC ABZ42662;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human endothelin A receptor nucleotide SEQ ID NO:115.  
XX  
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW G protein-coupled receptor modulator; antibody; immune-related disease;  
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KW immunological-related cell proliferative disease; autoimmune disease;  
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200261087-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 19-DEC-2001; 2001WO-US050107.  
XX  
PR 19-DEC-2000; 2000US-0257144P.  
XX  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX  
PI Burmer GC, Roush CL, Brown JP;  
XX  
DR WPI; 2003-046718/04.  
DR P-PSDB; ABP81816.  
XX  
PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
PT autoimmune diseases.  
XX  
PS Disclosure; Fig 1; 523pp; English.  
XX  
CC The present invention describes antigenic peptides (I) comprising: (a)  
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
CC acids. Also described: (1) an assay for the detection of a particular G  
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
CC and (2) an isolated antibody having high specificity and high affinity or  
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
CC antibody against a particular GPCR, and in the production of specific  
CC antibodies. The peptides and antibodies are also useful for detecting the  
CC presence or absence of corresponding GPCRs. The antigenic peptides for  
CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
CC treating immune-related diseases, growth-related diseases, cell  
CC regeneration-related disease, immunological-related cell proliferative  
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory

CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
CC exemplification of the present invention

XX

SQ Sequence 4105 BP; 1138 A; 859 C; 845 G; 1263 T; 0 U; 0 Other;

Query Match 100.0%; Score 4105; DB 7; Length 4105;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GAATTCGCGGCCGCCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60
        |||
Db      1 GAATTCGCGGCCGCCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60

Qy     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTCGTGCGAGCCCT 120
        |||
Db     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTCGTGCGAGCCCT 120

Qy    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
        |||
Db    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240
        |||
Db    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy    241 GCAGTGCCCAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300
        |||
Db    241 GCAGTGCCCAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
        |||
Db    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360

Qy    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420
        |||
Db    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420

Qy    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTCCTCAAATTTGCCT 480
        |||
Db    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTCCTCAAATTTGCCT 480

Qy    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
        |||
Db    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540

Qy    541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 600
        |||
Db    541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 600

Qy    601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660
        |||
Db    601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660
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Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTCTGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTCTGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560

Db	1501	 CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	 CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	 TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	 CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	 GAGCAGCCATAAGGACAGCATGAACTGACCACCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTTCTCTGATC	1860
Db	1801	 AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	 CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTACATA	1980
Db	1921	 CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	 TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	 AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Db	2101	 CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	 AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTCA	2280
Db	2221	 ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	 TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAA	2400

Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240

Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080

Qy 4081 TAAAATAAAAGTTTACAGAAACCTT 4105  
 |||  
 Db 4081 TAAAATAAAAGTTTACAGAAACCTT 4105

RESULT 4

AAQ34583

ID AAQ34583 standard; DNA; 4105 BP.

XX

AC AAQ34583;

XX

DT 25-MAR-2003 (revised)

DT 11-MAY-1993 (first entry)

XX

DE ETa receptor gene.

XX

KW Human; ETa; ETb; endothelin; receptor; transmembrane domain; N tail;  
 KW extracellular; cytoplasmic; C tail; post translational; bovine;  
 KW modification; ET-1 receptor; antagonist; circulatory system; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
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FT	CDS	485. .1768
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FT		/*tag= a
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FT	sig_peptide	485. .544
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FT		/*tag= b
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FT	mat_peptide	545. .1765
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FT		/*tag= c
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FT	misc_feature	1972. .1976
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FT		/*tag= e
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FT		/function= "Related with mRNA instability"
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FT	misc_feature	2059. .2063
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FT		/*tag= f
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FT		/function= "Related with mRNA instability"
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FT	misc_feature	2309. .2313
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FT		/function= "Related with mRNA instability"
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FT	misc_feature	2386. .2390
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FT		/function= "Related with mRNA instability"
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FT	misc_feature	2680. .2684
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FT		/function= "Related with mRNA instability"
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FT	misc_feature	3252. .3256
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FT		/function= "Related with mRNA instability"
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FT	misc_feature	3944. .3948
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FT		/*tag= k
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FT		/function= "Related with mRNA instability"
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FT	polyA_signal	4084. .4089
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FT		/*tag= d
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XX

PN EP522868-A1.

XX

PD 13-JAN-1993.

XX



PF 10-JUL-1992; 92EP-00306347.  
 XX  
 PR 12-JUL-1991; 91JP-00172828.  
 XX  
 PA (SHIO ) SHIONOGI SEIYAKU KK.  
 XX  
 PI Imura H, Nakao K, Nakanishi S;  
 XX  
 DR WPI; 1993-010677/02.  
 DR P-PSDB; AAR30885.  
 XX  
 PT Human ETa and ETb endothelin receptors - for measuring endothelin and  
 PT screening for endothelin antagonists.  
 XX  
 PS Claim 6; Fig 1; 39pp; English.  
 XX  
 CC The sequences given in AAQ34583-84 encode the human ETa and ETb  
 CC endothelin receptors respectively. ETa is a 427 amino acid protein with a  
 CC molecular weight of 48,726. ETb comprises 442 amino acids and has a  
 CC molecular weight of 49,629. ETa has a higher affinity for endothelin (ET)  
 CC -1 and ET-2, whereas ETb has no selectivity for ET-1, ET-2 or ET-3. The  
 CC receptors each contain seven transmembrane domains and have an  
 CC extracellular N tail and a cytoplasmic C tail. There are several  
 CC potential sites for post translational modification, these sites are  
 CC identical to those of bovine ET-1 receptor. ETa cDNA is 91.2% homologous  
 CC to bovine ET-1 receptor cDNA and ETb cDNA is 61.1% homologous to that of  
 CC bovine ETa-receptor. The receptor proteins are useful as reagents for  
 CC measuring the amount of ET or screening for antagonists of the ET  
 CC receptor when studying the circulatory system. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 4105 BP; 1138 A; 860 C; 844 G; 1263 T; 0 U; 0 Other;

Query Match 100.0%; Score 4103.4; DB 2; Length 4105;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GAATTCGCGGCCCGCTCTTGCGGTCCCAGAGTGGAGTGGAAAGGTCTGGAGCTTTGGGAGG	60
Db	1	GAATTCGCGGCCCGCTCTTGCGGTCCCAGAGTGGAGTGGAAAGGTCTGGAGCTTTGGGAGG	60
Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTTCGTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTTCGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300

Qy	301	CGGAGCCCGGGACACCGGCCACCC'TCCGCGCCACCCACCC'TCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCC'TCCGCGCCACCCACCC'TCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCCCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCCCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200

Db	1141	 TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	 TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG	1440
Db	1381	 GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1501	 CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	 CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	 TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAACAACCACAACACAGACCG	1740
Db	1681	 CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	 GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	 AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	 CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	 CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040

Db 1981 TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT 2040

Qy 2041 AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGG 2100  
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Db 2041 AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGG 2100

Qy 2101 CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACCTGGTCACCATGAAACTTTAG 2160  
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Db 2101 CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACCTGGTCACCATGAAACTTTAG 2160

Qy 2161 AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA 2220  
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Db 2161 AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA 2220

Qy 2221 ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA 2280  
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Db 2221 ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA 2280

Qy 2281 TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAAAGACAAA 2340  
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Db 2281 TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAAAGACAAA 2340

Qy 2341 AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTTATTTTTTAAA 2400  
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Db 2341 AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTTATTTTTTAAA 2400

Qy 2401 ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA 2460  
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Db 2401 ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA 2460

Qy 2461 TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA 2520  
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Db 2461 TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA 2520

Qy 2521 ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC 2580  
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Db 2521 ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC 2580

Qy 2581 TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA 2640  
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Db 2581 TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA 2640

Qy 2641 AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT 2700  
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Db 2641 AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT 2700

Qy 2701 TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG 2760  
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Db 2701 TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG 2760

Qy 2761 ATGATTTCGGAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT 2820  
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Db 2761 ATGATTTCGGAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT 2820

Qy 2821 CACCTCCTATTCTCTTAATTTTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA 2880  
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Db 2821 CACCTCCTATTCTCTTAATTTTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA 2880

Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720

Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTG	4080
Qy	4081	TAAAATAAAAGTTTACAGAAACCTT	4105
Db	4081	TAAAATAAAAGTTTACAGAAACCTT	4105

RESULT 5

AAA38341

ID AAA38341 standard; DNA; 4105 BP.

XX

AC AAA38341;

XX

DT 21-AUG-2000 (first entry)

XX

DE Human endothelin receptor type A gene coding region.

XX

KW Endothelin receptor type A gene; coding region; polymorphism;

KW polymorphic marker; cardiovascular disease; myocardial infarction;

KW unstable angina; hypertension; atherosclerosis; stroke; prognosis;

KW drug screening; treatment outcome; human; ds.

XX

OS Homo sapiens.

XX

PN WO200022166-A2.

XX

PD 20-APR-2000.

XX

PF 13-OCT-1999; 99WO-IB001678.

XX

PR 14-OCT-1998; 98US-0104286P.

PR 14-OCT-1998; 98US-0104302P.

XX

PA (EURO-) EURONA MEDICAL AB.

XX

PI Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;  
 XX  
 DR WPI; 2000-318010/27.  
 XX  
 PT Assessing cardiovascular status in humans involves comparing test  
 PT polymorphic pattern comprising polymorphic positions within genes  
 PT encoding specific proteins, with reference polymorphic pattern.  
 XX  
 PS Disclosure; Page 125-126; 126pp; English.  
 XX  
 CC The invention relates to a novel method of assessing the cardiovascular  
 CC status in an individual and to newly identified polymorphisms in the  
 CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II  
 CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,  
 CC aldosterone synthase, endothelin receptor type A and beta-adrenergic  
 CC receptors 1 and 2. The method comprises determining the sequence at one  
 CC or more polymorphic positions within these genes, and comparing the  
 CC pattern of polymorphisms from the individual with a reference polymorphic  
 CC pattern obtained from a population of individuals exhibiting a  
 CC predetermined cardiovascular disease status. The polymorphic markers are  
 CC useful for determining the predisposition of an individual to  
 CC cardiovascular disorders such as myocardial infarction, unstable angina,  
 CC hypertension, atherosclerosis and stroke. They are also useful for  
 CC predicting the likely cardiovascular status of a patient given a  
 CC treatment regimen comprising administration of cardiovascular drugs  
 CC (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-  
 CC blockers) or calcium channel blockers). One or more polymorphic markers  
 CC provides a basis for predicting the outcome of a treatment regimen.  
 CC Fragments of the genes comprising a polymorphic site may be used as  
 CC primers and probes for detecting genetic polymorphisms or in molecular  
 CC library arrays for high throughput screening. The genes, and the proteins  
 CC they encode are useful in the screening of potential cardiovascular  
 CC drugs. Determination of an individual's polymorphic pattern reduces or  
 CC eliminates trial and error in selecting a treatment for a particular  
 CC individual cardiovascular patient. It also provides the ability to  
 CC eliminate patients from clinical trials who are predicted to be non-  
 CC responsive, or at a risk for an adverse response, to a particular  
 CC treatment regimen. Adverse results in an early trial can be evaluated to  
 CC identify polymorphic patterns so that the adverse results can be  
 CC correlated with a sub-population of the test population, permitting  
 CC exclusion of such sub-populations from the treatment group. Beneficial  
 CC drugs can be approved for use in the appropriate population, thereby  
 CC decreasing the number of patients required for a clinical trial, which in  
 CC turn decreases the duration and cost of such trials. The present sequence  
 CC represents the human endothelin receptor type A gene coding region  
 CC (GenBank S57498). The polymorphic sites identified are 969C/T, 1005A/G,  
 CC 1146A/G and 2485T/C  
 XX  
 SQ Sequence 4105 BP; 1138 A; 859 C; 843 G; 1263 T; 0 U; 2 Other;  
  
 Query Match 100.0%; Score 4103; DB 3; Length 4105;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
 Qy 1 GAATTCGCGGCCCGCCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 GAATTCGCGGCCCGCCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCCTCCGGAGTTTCTTTTTTCGTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCCTCCGGAGTTTCTTTTTTCGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCGAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCGAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTCTCCGGCTTCTCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTCTCCGGCTTCTCTC	360
Qy	361	TGGCCCGAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCGAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCCCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCCCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900



Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCAC'TGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCAC'TGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAANNAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAAC'TGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAAC'TGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAAC'TTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAAC'TTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800

Db	1741	 GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	 AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	 CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	 CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTGAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	 TTCTGCGTGTTGTATTGAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGG	2100
Db	2041	 AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Db	2101	 CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	 AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTACA	2280
Db	2221	 ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTACA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAAGTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	 TAATAGCCTAACATGATTATTTGAAGTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCCTATTTATTTTTTTTAA	2400
Db	2341	 AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCCTATTTATTTTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	 ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	 TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	 ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTGTATGA	2640

Db	2581	TTCAATCAGATAGTTCTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCACCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCCCACAGTGACTTTTGTGTTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCCCACAGTGACTTTTGTGTTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480

Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Qy	4081	TAAAATAAAAGTTTACAGAAACCTT	4105
Db	4081	TAAAATAAAAGTTTACAGAAACCTT	4105

# RESULT 6

ACA56659

ID ACA56659 standard; cDNA; 4079 BP.

XX

AC ACA56659;

XX

DT 06-JUN-2003 (first entry)

XX

DE Human signalling pathway polynucleotide probe SEQ ID NO 1257.

XX

KW Human; probe; ss; array element; Parkinson's disease;

KW signalling pathway population; cancer; adenocarcinoma; leukaemia;  
 KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6500938-B1.  
 XX  
 PD 31-DEC-2002.  
 XX  
 PF 30-JAN-1998; 98US-00016434.  
 XX  
 PR 30-JAN-1998; 98US-00016434.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Au-Young J, Seilhamer JJ;  
 XX  
 DR WPI; 2003-352189/33.  
 XX  
 PT Combination of polynucleotide probes, useful as array elements in a  
 PT microarray for monitoring the expression of a number of target  
 PT polynucleotides.  
 XX  
 PS Claim 1; SEQ ID NO 1257; 65pp; English.  
 XX  
 CC The invention relates to a combination which, comprises a number of  
 CC polynucleotide probes comprising a sequence selected from one of the 1490  
 CC sequences mentioned in the specification. The combination is useful as an  
 CC array element in a microarray for monitoring the expression of a number  
 CC of target polynucleotides. The microarray is particularly useful in the  
 CC diagnosis and treatment of cancer and immunopathology and neuropathology.  
 CC The microarray is useful in diagnostics and treatment regimens, drug  
 CC discovery and development, toxicological and carcinogenicity studies,  
 CC forensics and pharmacogenomics. The microarray is also useful for  
 CC monitoring progression of diseases and for developing sophisticated  
 CC profiles for the effects of currently available therapeutic drugs. The  
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
 CC and genomic fragments and in research and diagnostic applications. The  
 CC array can detect changes in expression in a large number of genes coding  
 CC for different signaling pathway populations which can be used to diagnose  
 CC various diseases including cancer e.g. adenocarcinoma and leukaemia,  
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
 CC and Parkinson's disease. The present sequence represents a polynucleotide  
 CC probe of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=06500938B1  
 XX  
 SQ Sequence 4079 BP; 1125 A; 856 C; 842 G; 1256 T; 0 U; 0 Other;  
  
 Query Match 99.4%; Score 4079; DB 7; Length 4079;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4079; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 5 TCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGGAGAC 64  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 TCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGGAGAC 60

Qy	65	GGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCTCGCG	124
Db	61	GGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCTCGCG	120
Qy	125	CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC	184
Db	121	CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC	180
Qy	185	CATCCCACCCGGTCGTGCGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAG	244
Db	181	CATCCCACCCGGTCGTGCGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAG	240
Qy	245	TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA	304
Db	241	TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA	300
Qy	305	GCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTCTCCGGCTTCTCTGGC	364
Db	301	GCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTCTCCGGCTTCTCTGGC	360
Qy	365	CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAAA	424
Db	361	CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAAA	420
Qy	425	AGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTCCTCAAATTTGCCTCAAG	484
Db	421	AGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTCCTCAAATTTGCCTCAAG	480
Qy	485	ATGGAAACCCCTTTCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	544
Db	481	ATGGAAACCCCTTTCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	540
Qy	545	GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTCACCACTTTT	604
Db	541	GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTCACCACTTTT	600
Qy	605	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	664
Db	601	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	660
Qy	665	AGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAAA	724
Db	661	AGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAAA	720
Qy	725	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACT	784
Db	721	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACT	780
Qy	785	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
Db	781	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	840
Qy	845	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	841	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	900

Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	901	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	960
Qy	965	TTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	961	TTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1020
Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCCTTTG	1084
Db	1021	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCCTTTG	1080
Qy	1085	GTAAGTGCATTTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCCCTGAA	1144
Db	1081	GTAAGTGCATTTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCCCTGAA	1140
Qy	1145	GCGATTGGCTTCGTCATGGTACCC'TTTGAATATAGGGGTGAACAGCATAAAACTGTATG	1204
Db	1141	GCGATTGGCTTCGTCATGGTACCC'TTTGAATATAGGGGTGAACAGCATAAAACTGTATG	1200
Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTTCACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	1201	CTCAATGCCACATCAAAATTCATGGAGTTCACCAAGATGTAAAGGACTGGTGGCTCTTC	1260
Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1324
Db	1261	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1320
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384
Db	1321	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1380
Qy	1385	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTGGTTC	1444
Db	1381	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTGGTTC	1440
Qy	1445	CCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGA	1504
Db	1441	CCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGA	1500
Qy	1505	TGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG	1564
Db	1501	TGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG	1560
Qy	1565	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1624
Db	1561	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1620
Qy	1625	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCATG	1684
Db	1621	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCATG	1680
Qy	1685	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1744
Db	1681	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1740
Qy	1745	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATATC	1804

Db	1741	 AGCCATAAGGACAGCATGAAGTACCACCCTTAGAAGCACTCCTCGGTACTCCCATAATC	1800
Qy	1805	CTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1864
Db	1801	 CTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1860
Qy	1865	TTCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1924
Db	1861	 TTCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1920
Qy	1925	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1984
Db	1921	 TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1980
Qy	1985	GCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2044
Db	1981	 GCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2040
Qy	2045	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2104
Db	2041	 GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2100
Qy	2105	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAACTTTAGAGAT	2164
Db	2101	 CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAACTTTAGAGAT	2160
Qy	2165	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2224
Db	2161	 TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2220
Qy	2225	GGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2284
Db	2221	 GGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2280
Qy	2285	AGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAAAATA	2344
Db	2281	 AGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAAAATA	2340
Qy	2345	GTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCCTATTTATTTTTTAAACAC	2404
Db	2341	 GTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCCTATTTATTTTTTAAACAC	2400
Qy	2405	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2464
Db	2401	 AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2460
Qy	2465	GCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2524
Db	2461	 GCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2520
Qy	2525	TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTCA	2584
Db	2521	 TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTCA	2580
Qy	2585	ATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAAA	2644



Db	2581	ATCAGATAGTTCTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAAA	2640
Qy	2645	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCAG	2704
Db	2641	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCAG	2700
Qy	2705	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2764
Db	2701	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2760
Qy	2765	TTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2824
Db	2761	TTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2820
Qy	2825	TCCTATTCTCTTAATTTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2884
Db	2821	TCCTATTCTCTTAATTTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2880
Qy	2885	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2944
Db	2881	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2940
Qy	2945	AATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTTCTGGGGTTTTTCAG	3004
Db	2941	AATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTTCTGGGGTTTTTCAG	3000
Qy	3005	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGCC	3064
Db	3001	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGCC	3060
Qy	3065	CACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3124
Db	3061	CACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3120
Qy	3125	TCTTTTACTAGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATTT	3184
Db	3121	TCTTTTACTAGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATTT	3180
Qy	3185	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3244
Db	3181	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3240
Qy	3245	TGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCT	3304
Db	3241	TGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCT	3300
Qy	3305	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3364
Db	3301	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3360
Qy	3365	GCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3424
Db	3361	GCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3420
Qy	3425	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3484
Db	3421	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3480

Qy	3485	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3544
Db	3481	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3540
Qy	3545	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3604
Db	3541	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3600
Qy	3605	TGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3664
Db	3601	TGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3660
Qy	3665	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3724
Db	3661	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3720
Qy	3725	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCGCATC	3784
Db	3721	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCGCATC	3780
Qy	3785	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3844
Db	3781	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3840
Qy	3845	TTGTCTTTTTTTCAAGATGCTTTGTTTCCTTCATATGAAAAAATGCATTTTATAAATTC	3904
Db	3841	TTGTCTTTTTTTCAAGATGCTTTGTTTCCTTCATATGAAAAAATGCATTTTATAAATTC	3900
Qy	3905	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3964
Db	3901	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3960
Qy	3965	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTCAACAAGTA	4024
Db	3961	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTCAACAAGTA	4020
Qy	4025	ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAAGTGTA	4083
Db	4021	ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAAGTGTA	4079

# RESULT 7

ABK35492

ID ABK35492 standard; DNA; 2595 BP.

XX

AC ABK35492;

XX

DT 08-MAY-2002 (first entry)

XX

DE Human endometrial cancer related gene, EDNRA.

XX

KW Human; ds; gene; endometrial cancer; differential expression;

KW DNA microarray; protein microarray.

XX

OS Homo sapiens.

XX

PN WO200209573-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 31-JUL-2001; 2001WO-US024104.  
 XX  
 PR 31-JUL-2000; 2000US-0221735P.  
 XX  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
 XX  
 PI Mutter GL;  
 XX  
 DR WPI; 2002-179967/23.  
 DR P-PSDB; AAU84272.  
 XX  
 PT Diagnosing endometrial cancer comprises determining expression of nucleic  
 PT acid molecules or expression products that are differentially expressed  
 PT in normal and malignant endometrium.  
 XX  
 PS Claim 1; Page 60-62; 233pp; English.  
 XX  
 CC The invention relates to diagnosing endometrial cancer in a subject  
 CC suspected of having endometrial cancer comprising determining the  
 CC expression of a set of nucleic acid molecules or expression products in  
 CC an endometrial sample suspected of being cancerous, where the set of  
 CC nucleic acid molecules comprises at least 2 nucleic acid molecules  
 CC selected from 50 fully defined sequences as given in the specification.  
 CC The nucleic acids are used as an array of at least 2 of the 50 nucleic  
 CC acids bound to a solid substrate. Also included is a solid-phase protein  
 CC microarray comprising at least 2 antibodies or its antigen binding  
 CC fragments, that specifically bind at least 2 different polypeptides from  
 CC the 50 fully defined sequences as given in the specification, fixed to a  
 CC solid substrate. The methods and arrays are useful for the diagnosis of  
 CC endometrial cancer, selecting and monitoring treatment regimes and  
 CC identification of lead compounds useful for the treatment of endometrial  
 CC cancer. The present sequence is one of 50 genes differentially expressed  
 CC between cancerous and non-cancerous samples  
 XX  
 SQ Sequence 2595 BP; 788 A; 478 C; 459 G; 870 T; 0 U; 0 Other;

Query Match 60.2%; Score 2470; DB 6; Length 2595;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	1624	CCAGTCATGCCTCTGCTGCTGCTGTTACAGTCCAAAAGTCTGATGACCTCGGTCCCCAT	1683
Db	15	CCAGTCATGCCTCTGCTGCTGCTGTTACAGTCCAAAAGTCTGATGACCTCGGTCCCCAT	74
Qy	1684	GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG	1743
Db	75	GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG	134
Qy	1744	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	1803
Db	135	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	194
Qy	1804	CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGAATCTTCTCTGATCCTT	1863

Db	195	 CCTCTCGGAGAAAAAATCACAAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT	254
Qy	1864	CTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG	1923
Db	255	 CTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG	314
Qy	1924	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	1983
Db	315	 GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	374
Qy	1984	TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA	2043
Db	375	 TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA	434
Qy	2044	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTC AAGTACATGGCTA	2103
Db	435	 TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTC AAGTACATGGCTA	494
Qy	2104	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA	2163
Db	495	 GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA	554
Qy	2164	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2223
Db	555	 TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614
Qy	2224	TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	2283
Db	615	 TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAGACAAAAAT	2343
Db	675	 TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAAACA	2403
Db	735	 AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAAACA	794
Qy	2404	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	 CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	 GGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	2583
Db	915	 GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	 AATCAGATAGTTCTTTTTTACAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTTCA	2703

Db	1034	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	2763
Db	1094	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	1153
Qy	2764	ATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	ATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTGTTAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTC	2883
Db	1214	CTCCTATTCTCTTAATTTTTGTTAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTC	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	2943
Db	1274	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	AAATAATTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	3063
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
Db	1694	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	1753
Qy	3364	AGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	AGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	3483
Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	3543
Db	1874	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	1933

Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAAATT	3663
Db	1994	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAAATT	2053
Qy	3664	TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	3723
Db	2054	TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	3783
Db	2114	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	2173
Qy	3784	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTCCACACCATTTTGTTTAGACA	3843
Db	2174	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTCCACACCATTTTGTTTAGACA	2233
Qy	3844	ATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATT	3903
Db	2234	ATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATT	2293
Qy	3904	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	3963
Db	2294	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	2353
Qy	3964	CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT	4023
Db	2354	CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT	2413
Qy	4024	AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA	4083
Db	2414	AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA	2473
Qy	4084	AATAAAAGTTTACAGAAACCTT	4105
Db	2474	AATAAAAGTTTACAGAAACCTT	2495

RESULT 8

AAL39858

ID AAL39858 standard; DNA; 2595 BP.

XX

AC AAL39858;

XX

DT 05-SEP-2002 (first entry)

XX

DE Human allergy-associated gene SEQ ID No 30.

XX

KW Antiallergic; allergic disease; carboxypeptidase M; cathepsin C; CYP1B1;

KW endoserine A receptor; osteoblast-specific factor 2; DD96; gene therapy;

KW bronchial asthma; human; ds.

XX

OS Homo sapiens.

XX  
 PN WO200252006-A1.  
 XX  
 PD 04-JUL-2002.  
 XX  
 PF 21-DEC-2001; 2001WO-JP011287.  
 XX  
 PR 26-DEC-2000; 2000JP-00396166.  
 XX  
 PA (GENO-) GENOX RES INC.  
 XX  
 PI Ohtani N, Matsui K, Yoshida N, Sugita Y, Izuhara K;  
 XX  
 DR WPI; 2002-500763/53.  
 XX  
 PT Examining allergic diseases by changes in expression levels of six  
 PT allergy-associated genes inducible by stimulation e.g. of airway  
 PT epithelia cells with interleukin-4 or 13, also applicable in screening  
 PT compounds.  
 XX  
 PS Disclosure; Page 79-80; 106pp; Japanese.  
 XX  
 CC The invention relates to a novel method for examining allergic diseases,  
 CC comprising determining the expression level of a gene selected from  
 CC carboxypeptidase M, cathepsin C, endoserine A receptor, osteoblast-  
 CC specific factor 2, DD96 and CYP1B1 in the biological sample from a  
 CC patient, and comparing the expression level with that in the sample of a  
 CC healthy individual. The polynucleotides of the invention can be used to  
 CC treat disorders by gene therapy. The method is useful for examining  
 CC allergic diseases particularly bronchial asthma and its diagnosis, which  
 CC is also applicable in screening candidate compounds for remedies. This  
 CC polynucleotide sequence represents a human allergy-associated gene of the  
 CC invention  
 XX  
 SQ Sequence 2595 BP; 788 A; 478 C; 459 G; 870 T; 0 U; 0 Other;

Query Match 60.2%; Score 2470; DB 6; Length 2595;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	1624	CCAGTCATGCCTCTGCTGCTGCTGTTACCAAGTCTGATGACCTCGGTCCCCAT	1683
Db	15	CCAGTCATGCCTCTGCTGCTGCTGTTACCAAGTCTGATGACCTCGGTCCCCAT	74
Qy	1684	GAACGGAACAAGCATCCAGTGGAAGAACACGATCAAACAACCACAACACAGACCGGAG	1743
Db	75	GAACGGAACAAGCATCCAGTGGAAGAACACGATCAAACAACCACAACACAGACCGGAG	134
Qy	1744	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	1803
Db	135	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	194
Qy	1804	CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGAATCTCTTCTCTGATCCTT	1863
Db	195	CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGAATCTCTTCTCTGATCCTT	254
Qy	1864	CTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG	1923

Db	255	 CTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG	314
Qy	1924	GTTCATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	1983
Db	315	 GTTCATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	374
Qy	1984	TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA	2043
Db	375	 TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA	434
Qy	2044	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTA	2103
Db	435	 TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTA	494
Qy	2104	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTAGAGA	2163
Db	495	 GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTAGAGA	554
Qy	2164	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2223
Db	555	 TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614
Qy	2224	TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTAACTGCATAA	2283
Db	615	 TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	2343
Db	675	 TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTAAACA	2403
Db	735	 AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTAAACA	794
Qy	2404	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	 CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	 GGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	2583
Db	915	 GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	 AATCAGATAGTTCTTTTTTACAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	 ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	2763



Db	1094	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	1153
Qy	2764	ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTGTAAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTC	2883
Db	1214	CTCCTATTCTCTTAATTTTTGTAAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTC	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAAGTCAA	2943
Db	1274	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAAGTCAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	AAATAATTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	3063
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCAT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCAT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
Db	1694	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	1753
Qy	3364	AGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	AGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	3483
Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	3543
Db	1874	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993

Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	3663
Db	1994	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	2053
Qy	3664	TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	3723
Db	2054	TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCGCAT	3783
Db	2114	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCGCAT	2173
Qy	3784	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	3843
Db	2174	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	2233
Qy	3844	ATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATT	3903
Db	2234	ATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATT	2293
Qy	3904	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	3963
Db	2294	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	2353
Qy	3964	CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT	4023
Db	2354	CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT	2413
Qy	4024	AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA	4083
Db	2414	AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA	2473
Qy	4084	AATAAAAAGTTTACAGAAACCTT	4105
Db	2474	AATAAAAAGTTTACAGAAACCTT	2495

# RESULT 9

ABK94408

ID ABK94408 standard; DNA; 2595 BP.

XX

AC ABK94408;

XX

DT 27-AUG-2002 (first entry)

XX

DE DNA encoding endothelin receptor A (EDNRA), exon 8.

XX

KW Endothelin; EDN; endothelin converting enzyme; ECE; EDNRA;

KW endothelin receptor A; signaling system; cardiovascular disease;

KW coronary heart disease; hypertension; atherosclerosis; angiogenesis;

KW fatty acid metabolism; diabetes; familial hypercholesterolaemia;

KW forensic marker; transgenic animal; solid support; SNP;

KW cardiovascular regulator; gene; ds; single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers  
 FT variation replace(1830,G)  
 FT /\*tag= a  
 FT /standard\_name= "Single nucleotide polymorphism"  
 XX  
 PN WO200224747-A2.  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 31-AUG-2001; 2001WO-EP010087.  
 XX  
 PR 19-SEP-2000; 2000EP-00120123.  
 XX  
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
 XX  
 PI Brinkmann U, Hoffmeyer S;  
 XX  
 DR WPI; 2002-435060/46.  
 XX  
 PT Novel polynucleotide of the endothelin/endothelin converting  
 PT enzyme/receptors of endothelin and endothelin converting enzyme signaling  
 PT system associated with cardiovascular disease, useful for treating the  
 PT disease.  
 XX  
 PS Claim 1; Page; 190pp; English.  
 XX  
 CC The invention describes a polynucleotide (I) of the endothelin  
 CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)  
 CC signaling system which is associated with a cardiovascular disease. (I),  
 CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)  
 CC or (II) is useful for producing cells capable of expressing a molecular  
 CC variant polypeptide which is associated with a cardiovascular disease.  
 CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a  
 CC molecular variant gene comprising (I) is useful for identifying and  
 CC obtaining a pro-drug or drug capable of modulating the activity of a  
 CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system  
 CC or its gene product, or for identifying and obtaining an inhibitor of the  
 CC activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE  
 CC signaling system or its gene product. The isolated proteins and  
 CC polynucleotides encoding them are useful for preparation of a  
 CC pharmaceutical composition for treating a cardiovascular disease such as  
 CC coronary heart disease, hypertension, atherosclerosis, or related to  
 CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial  
 CC hypercholesterolaemia. The gene or a polynucleotide fragment of the  
 CC EDN/ECE/EDNR signaling system are useful as forensic markers, for  
 CC creating a transgenic animal and in creation of a solid support  
 CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or  
 CC host cells of the invention. This sequence encodes the cardioavascular  
 CC regulator Endothelin receptor A (EDNRA). Note: This sequence does not  
 CC appear in the specification but has been obtained from GenBank using  
 CC information given in the invention  
 XX  
 SQ Sequence 2595 BP; 788 A; 478 C; 459 G; 870 T; 0 U; 0 Other;

Query Match 60.2%; Score 2470; DB 6; Length 2595;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	1624	CCAGTCATGCCTCTGCTGCTGCTGTTACCAAGTCCAAAAGTCTGATGACCTCGGTCCCCAT	1683
Db	15	CCAGTCATGCCTCTGCTGCTGCTGTTACCAAGTCCAAAAGTCTGATGACCTCGGTCCCCAT	74
Qy	1684	GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG	1743
Db	75	GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG	134
Qy	1744	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	1803
Db	135	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	194
Qy	1804	CCTCTCGGAGAAAAAATCACAAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT	1863
Db	195	CCTCTCGGAGAAAAAATCACAAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT	254
Qy	1864	CTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTCCAAAACCGCAAGGTAGACTG	1923
Db	255	CTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTCCAAAACCGCAAGGTAGACTG	314
Qy	1924	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTACATATTC	1983
Db	315	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTACATATTC	374
Qy	1984	TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA	2043
Db	375	TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA	434
Qy	2044	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAGTACATGGCTA	2103
Db	435	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAGTACATGGCTA	494
Qy	2104	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTAGAGA	2163
Db	495	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTAGAGA	554
Qy	2164	TTAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2223
Db	555	TTAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614
Qy	2224	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	2283
Db	615	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	2343
Db	675	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTCCACGTCCTACTATTTATTTTTTAAAACA	2403
Db	735	AGTATTCAGGTGAGCAATTAGATTAGTATTTCCACGTCCTACTATTTATTTTTTAAAACA	794
Qy	2404	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854

Qy	2464	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	2583
Db	915	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTACAAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	AATCAGATAGTTCTTTTTTACAAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	2763
Db	1094	GTGCACTGTATATAGAAGTCTAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	1153
Qy	2764	ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTGTTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	2883
Db	1214	CTCCTATTCTCTTAATTTTTGTTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	2943
Db	1274	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	AAATAATTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGC	3063
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363

Db	1694	 TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	1753
Qy	3364	AGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	 AGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTGTGTTGGTTGGTTGG	3483
Db	1814	 GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTGTGTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	3543
Db	1874	 TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	 TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAAAT	3663
Db	1994	 CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAAAT	2053
Qy	3664	TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	3723
Db	2054	 TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCGCAT	3783
Db	2114	 GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCGCAT	2173
Qy	3784	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTCCACACCATTTTGTGTTAGACA	3843
Db	2174	 CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTCCACACCATTTTGTGTTAGACA	2233
Qy	3844	ATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAAT	3903
Db	2234	 ATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAAT	2293
Qy	3904	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	3963
Db	2294	 CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	2353
Qy	3964	CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT	4023
Db	2354	 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT	2413
Qy	4024	AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA	4083
Db	2414	 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA	2473
Qy	4084	AATAAAAGTTTACAGAAACCTT	4105
Db	2474	 AATAAAAGTTTACAGAAACCTT	2495

AAA34793

ID AAA34793 standard; DNA; 1868 BP.

XX

AC AAA34793;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide SEQ ID NO:2482.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX

OS Homo sapiens.

XX

PN WO200009525-A2.

XX

PD 24-FEB-2000.

XX

PF 03-AUG-1999; 99WO-US017712.

XX

PR 03-AUG-1998; 98US-0095212P.

XX

PA (UYEC-) UNIV EAST CAROLINA.

XX

PI Nyce JW;

XX

DR WPI; 2000-205971/18.

XX

PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstruction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.

XX

PS Disclosure; Page 645-646; 1343pp; English.

XX

CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing

CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing

XX

SQ Sequence 1868 BP; 512 A; 419 C; 389 G; 548 T; 0 U; 0 Other;

Query Match 44.3%; Score 1819.6; DB 3; Length 1868;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy	421	AAAAAGTGAAGGTGTAAAGCAGCACAAGTGCAATAAGAGATATTTTCCTCAAATTTGCCT	480
Db	10	AAAAAGTGAAGGTGTAAAGCAGCACAAGTGCAATAAGAGATATTTTCCTCAAATTTGCCT	69
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTGGATGTGTAAT	540
Db	70	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTGGATGTGTAAT	129
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	130	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	189
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	190	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	249
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	250	ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	309
Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGC	780
Db	310	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGC	369
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	370	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	429
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	430	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	489
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	490	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	549
Qy	961	GCTGTTCCCTTTTTCAGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	550	GCTGTTCCCTTTTTCAGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	609
Qy	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	1080



Db	610	 TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCC	669
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	670	 TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	729
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	730	 TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	789
Qy	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	790	 TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	849
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	850	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	909
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	910	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	969
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	970	 GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1029
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1030	 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAGATGGACAAGAA	1089
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1090	 CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1149
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1150	 CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1209
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1210	 TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1269
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1270	 CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1329
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1330	 GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1389
Qy	1801	AATCCTCTCGGAGAAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1390	 AATCCTCTCGGAGAAAAAAATCACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATC	1449
Qy	1861	CTTCTTCCTTAATTCACCTCCACACCCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAG	1919

Db 1450 CTTCTTCCTTAATTCACCTCCACACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGGTAG 1509  
 Qy 1920 ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT 1979  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1510 ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT 1569  
 Qy 1980 ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT 2039  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1570 ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT 1629  
 Qy 2040 TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAGTACATG 2099  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1630 TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAGTACATG 1689  
 Qy 2100 GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAAACTTTA 2159  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1690 GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAAACTTTA 1749  
 Qy 2160 GAGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA 2218  
 |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||  
 Db 1750 GAGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTTTGTCTTCAGCCAAACA 1809  
 Qy 2219 CAATATGGGCTCAGGTCACTTTTATTTGAAATGTCATT'TGGTGCCAGTAT 2268  
 |||||||||||| ||||||||||||||||||||||||||||||||||||  
 Db 1810 CAATATGGGCTCAAGTCACTTTTATTTGAAATGTCATT'TGGTGCCAGTAT 1859

RESULT 11

AAA34781

ID AAA34781 standard; DNA; 1868 BP.

XX

AC AAA34781;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide SEQ ID NO:2470.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX

OS Homo sapiens.

XX

PN WO200009525-A2.

XX

PD 24-FEB-2000.

XX

PF 03-AUG-1999; 99WO-US017712.

XX

PR 03-AUG-1998; 98US-0095212P.

XX

PA (UYEC-) UNIV EAST CAROLINA.

XX  
PI Nyce JW;  
XX  
DR WPI; 2000-205971/18.  
XX  
PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
PS Disclosure; Page 606-607; 1343pp; English.  
XX  
CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 1868 BP; 512 A; 419 C; 389 G; 548 T; 0 U; 0 Other;

Query Match 44.3%; Score 1819.6; DB 3; Length 1868;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCCTCAAATTTGCCT	480
Db	10	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCCTCAAATTTGCCT	69
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	70	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	129
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	130	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	189
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660

Db	190		TTTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	249
Qy	661		ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	250		ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	309
Qy	721		CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	310		CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	369
Qy	781		AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	370		AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	429
Qy	841		AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	430		AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	489
Qy	901		TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	490		TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	549
Qy	961		GCTGTTCCCTTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	550		GCTGTTCCCTTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	609
Qy	1021		TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	1080
Db	610		TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	669
Qy	1081		TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	670		TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	729
Qy	1141		TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	730		TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	789
Qy	1201		TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	790		TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	849
Qy	1261		CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	850		CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	909
Qy	1321		TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	910		TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	969
Qy	1381		GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTGCTG	1440
Db	970		GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTGCTG	1029
Qy	1441		GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500

Db	1030	GTTCCCTCTTCATTTAAGCCGTATATTGAAGAAACTGTGTATAACGAGATGGACAAGAA	1089
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1090	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1149
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1150	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1209
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1210	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1269
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1740
Db	1270	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1329
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1330	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1389
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1390	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATC	1449
Qy	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAA--GGTAG	1919
Db	1450	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGGTAG	1509
Qy	1920	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1979
Db	1510	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1569
Qy	1980	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	2039
Db	1570	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	1629
Qy	2040	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	2099
Db	1630	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	1689
Qy	2100	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAAACTTTA	2159
Db	1690	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAAACTTTA	1749
Qy	2160	GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA	2218
Db	1750	GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTTGTCTTCAGCCAAACA	1809
Qy	2219	CAATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTAT	2268
Db	1810	CAATATGGGCTCAAGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTAT	1859

ID AAF20915 standard; DNA; 1868 BP.  
XX  
AC AAF20915;  
XX  
DT 14-MAR-2001 (first entry)  
XX  
DE Human endothelin receptor A polynucleotide fragment #2482.  
XX  
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200062736-A2.  
XX  
PD 26-OCT-2000.  
XX  
PF 24-MAR-2000; 2000WO-US008020.  
XX  
PR 06-APR-1999; 99US-0127958P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-679539/66.  
XX  
PT Low adenosine (A) content antisense oligonucleotides which do not trigger  
PT adenosine receptors during metabolism, useful e.g. for treating cancers  
PT and respiratory obstructions.  
XX  
PS Disclosure; Page 244; 1592pp; English.  
XX  
CC The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors, CNS and peripheral nervous and non-nervous system peptide

CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention

XX

SQ Sequence 1868 BP; 512 A; 419 C; 389 G; 548 T; 0 U; 0 Other;

Query Match 44.3%; Score 1819.6; DB 3; Length 1868;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGAATAAGAGATATTTCTCCTCAAATTTGCCT	480
Db	10	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGAATAAGAGATATTTCTCCTCAAATTTGCCT	69
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	70	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	129
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	130	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	189
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	190	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	249
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	250	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	309
Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	310	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	369
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	370	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	429
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	430	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	489
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	490	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	549

Qy	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	550	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	609
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCC	1080
Db	610	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCC	669
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	670	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	729
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	730	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	789
Qy	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	790	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	849
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	850	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	909
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	910	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	969
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGCTG	1440
Db	970	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGCTG	1029
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1030	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAGATGGACAAGAA	1089
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1090	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1149
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1150	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1209
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1210	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1269
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1740
Db	1270	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1329
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1330	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1389
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860



Db	1390	 AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATC	1449
Qy	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAG	1919
Db	1450	 CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGGTAG	1509
Qy	1920	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1979
Db	1510	 ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1569
Qy	1980	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	2039
Db	1570	 ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	1629
Qy	2040	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	2099
Db	1630	 TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	1689
Qy	2100	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAAACTTTA	2159
Db	1690	 GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAAACTTTA	1749
Qy	2160	GAGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA	2218
Db	1750	 GAGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA	1809
Qy	2219	CAATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT	2268
Db	1810	 CAATATGGGCTCAAGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT	1859

RESULT 13

AAF20903

ID AAF20903 standard; DNA; 1868 BP.

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AC AAF20903;

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DT 14-MAR-2001 (first entry)

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DE Human low adenosine antisense oligonucleotide #2470.

XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.

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OS Homo sapiens.

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PN WO200062736-A2.

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Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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Db	10	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	69
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	70	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	129
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTCACCAC	600
Db	130	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTCACCAC	189
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	190	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	249
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	250	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	309
Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGC	780
Db	310	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGC	369
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGTGAT	840
Db	370	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGTGAT	429
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	430	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	489
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	490	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	549
Qy	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	550	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	609
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCC	1080
Db	610	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCC	669
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	670	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	729
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	730	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	789
Qy	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	790	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	849
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	850	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	909

Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	910	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	969
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGCTG	1440
Db	970	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGCTG	1029
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1030	GTTCCCTCTTCATTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAGATGGACAAGAA	1089
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1090	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1149
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1150	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1209
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1210	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1269
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1270	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1329
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1330	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1389
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1390	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATC	1449
Qy	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAG	1919
Db	1450	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGGTAG	1509
Qy	1920	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1979
Db	1510	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1569
Qy	1980	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	2039
Db	1570	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	1629
Qy	2040	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	2099
Db	1630	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	1689
Qy	2100	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAAACTTTA	2159
Db	1690	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAAACTTTA	1749

QY 2160 GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA 2218  
 |||  
 Db 1750 GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACA 1809  
 |||  
 QY 2219 CAATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTAT 2268  
 |||  
 Db 1810 CAATATGGGCTCAAGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTAT 1859

RESULT 14

ABZ96609

ID ABZ96609 standard; DNA; 1868 BP.

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AC ABZ96609;

XX

DT 17-OCT-2003 (first entry)

XX

DE Human endothelin receptor A nucleic acid.

XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

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OS Homo sapiens.

XX

PN WO200285308-A2.

XX

PD 31-OCT-2002.

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PF 23-APR-2002; 2002WO-US013135.

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PR 24-APR-2001; 2001US-0286137P.

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PA (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX

DR WPI; 2003-229219/22.

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PT Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.

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PS Disclosure; SEQ ID NO 11851; 872pp; English.

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CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 1868 BP; 512 A; 419 C; 389 G; 548 T; 0 U; 0 Other;

Query Match 44.3%; Score 1819.6; DB 7; Length 1868;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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Qy      421 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCTCAAATTTGCCT 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCTCAAATTTGCCT 69

Qy      481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      70 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 129

Qy      541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 600
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      130 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 189

Qy      601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      190 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 249

Qy      661 ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT 720
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      250 ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT 309

Qy      721 CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC 780
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      310 CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC 369

Qy      781 AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT 840
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      370 AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT 429

Qy      841 AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT 900
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      430 AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT 489

Qy      901 TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA 960
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      490 TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA 549

Qy      961 GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT 1020
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Db	550	 GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	609
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGGAATTGGGATTCC	1080
Db	610	 TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGGAATTGGGATTCC	669
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	670	 TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	729
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	730	 TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	789
Qy	1201	TATGCTCAATGCCACATCAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	790	 TATGCTCAATGCCACATCAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	849
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	850	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	909
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	910	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	969
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	970	 GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1029
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1030	 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAGATGGACAAGAA	1089
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1090	 CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1149
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1150	 CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1209
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1210	 TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAAGTCCAAAAGTCTGATGACCTCGGTCCC	1269
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1270	 CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1329
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Db	1330	 GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1389
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860

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Qy	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAG	1919
Db	1450	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAG	1509
Qy	1920	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1979
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Qy	1980	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	2039
Db	1570	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	1629
Qy	2040	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	2099
Db	1630	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	1689
Qy	2100	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTA	2159
Db	1690	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTA	1749
Qy	2160	GAGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA	2218
Db	1750	GAGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTTGTCTTCAGCCAAACA	1809
Qy	2219	CAATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT	2268
Db	1810	CAATATGGGCTCAAGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT	1859

# RESULT 15

ABZ96597

ID ABZ96597 standard; DNA; 1868 BP.

XX

AC ABZ96597;

XX

DT 17-OCT-2003 (first entry)

XX

DE Human endothelin receptor A nucleic acid.

XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

XX

OS Homo sapiens.

XX

PN WO200285308-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013135.

XX

PR 24-APR-2001; 2001US-0286137P.



XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 11839; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1868 BP; 512 A; 419 C; 389 G; 548 T; 0 U; 0 Other;

Query Match 44.3%; Score 1819.6; DB 7; Length 1868;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTTCCTCAAATTTGCCT	480
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Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	70	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	129
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	130	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	189
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
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Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
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Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	310	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	369
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
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Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	430	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	489
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Db	490	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	549
Qy	961	GCTGTTCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	550	GCTGTTCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	609
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCC	1080
Db	610	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCC	669
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Db	670	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	729
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Db	790	TATGCTCAATGCCACATCAAATTCATGGAGTTCACCAAGATGTAAAGGACTGGTGGCT	849
Qy	1261	CTTCGGGTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
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Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	910	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	969
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTGCTG	1440
Db	970	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTGCTG	1029
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTATAACGAAATGGACAAGAA	1500
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Db	1090	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1149
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Db	1270	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1329
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Qy	1920	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1979
Db	1510	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1569
Qy	1980	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	2039
Db	1570	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	1629
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Db	1630	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	1689
Qy	2100	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTA	2159
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Qy	2160	GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGA--TTTTTTGTCCTTCAGCCAAACA	2218
Db	1750	GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTTGTCCTTCAGCCAAACA	1809
Qy	2219	CAATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTAT	2268
Db	1810	CAATATGGGCTCAAGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTAT	1859

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Job time : 1448.24 secs

OM nucleic - nucleic search, using sw model

Run on: May 14, 2004, 00:25:48 ; Search time 254.426 Seconds  
(without alignments)  
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Perfect score: 4105  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	4079	99.4	4079	4	US-09-016-434-1257	Sequence 1257, Ap
3	406.2	9.9	1321	4	US-09-175-658B-20	Sequence 20, Appl
4	395.8	9.6	1470	4	US-09-016-434-1203	Sequence 1203, Ap
5	395.8	9.6	1873	3	US-08-910-864-13	Sequence 13, Appl
6	395.8	9.6	4301	4	US-08-121-446-3	Sequence 3, Appli
7	101.8	2.5	1700	5	PCT-US92-02091-1	Sequence 1, Appli
8	91	2.2	1726	4	US-09-016-434-1215	Sequence 1215, Ap
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	14	65.8	1.6	1584	5	PCT-US92-02091-5	Sequence 5, Appli
	15	63.6	1.5	1563	1	US-08-279-590A-1	Sequence 1, Appli
	16	63.6	1.5	1563	1	US-08-910-092-1	Sequence 1, Appli
	17	55.6	1.4	11015	4	US-10-204-708-55	Sequence 55, Appl
c	18	51.4	1.3	3095	6	5231168-1	Patent No. 5231168
	19	50.2	1.2	832	4	US-09-621-976-2813	Sequence 2813, Ap
	20	49.6	1.2	505	4	US-09-621-976-15639	Sequence 15639, A
	21	48.8	1.2	5152	4	US-10-204-708-73	Sequence 73, Appl
	22	48.6	1.2	6656	4	US-10-204-708-75	Sequence 75, Appl
c	23	48.4	1.2	11049	4	US-10-204-708-22	Sequence 22, Appl
c	24	47.8	1.2	832	4	US-09-621-976-2813	Sequence 2813, Ap
	25	47.4	1.2	1842	4	US-09-170-496D-91	Sequence 91, Appl
	26	47.4	1.2	1842	4	US-09-170-496D-211	Sequence 211, App
	27	46.8	1.1	1238	4	US-09-761-962A-2	Sequence 2, Appli
	28	46.8	1.1	1257	4	US-09-761-962A-5	Sequence 5, Appli
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	34	46.8	1.1	1610	4	US-09-761-962A-16	Sequence 16, Appl
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#### ALIGNMENTS

#### RESULT 1

US-08-121-446-1

; Sequence 1, Application US/08121446

; Patent No. 6313276

; GENERAL INFORMATION:

; APPLICANT: IMURA, HIROO

; APPLICANT: NAKAO, KAZUWA

; APPLICANT: NAKANISHI, SHIGETADA

; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,446
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,684
; FILING DATE: 10-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 29900-20324.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4105 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 485..1768
; FEATURE:
; NAME/KEY: mat_peptide
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Db    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

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Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200

Db	1141	 TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	 TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGCTG	1440
Db	1381	 GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1501	 CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	 CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	 TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	 CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	 GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTTCTCTGATC	1860
Db	1801	 AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	 CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	 CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040



Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880

Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
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Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGT'TGGT'	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGT'TGGT'	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720

Qy 3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCTACTGGCG 3780  
 |||  
 Db 3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCTACTGGCG 3780  
 |||  
 Qy 3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTACACCATTTTGTTTAG 3840  
 |||  
 Db 3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTACACCATTTTGTTTAG 3840  
 |||  
 Qy 3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA 3900  
 |||  
 Db 3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA 3900  
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 Qy 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960  
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 Db 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960  
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 Qy 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080  
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RESULT 2

US-09-016-434-1257

; Sequence 1257, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

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; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1257:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g219649
US-09-016-434-1257

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Query Match          99.4%; Score 4079; DB 4; Length 4079;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4079; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      5 TCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGGAGAC 64
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Db      1 TCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGGAGAC 60

Qy     65 GGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCTCGCG 124
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCTCGCG 120

Qy    125 CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC 184
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC 180

Qy    185 CATCCACCCGGTCGTGCGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAG 244
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CATCCACCCGGTCGTGCGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAG 240

Qy    245 TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA 304
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA 300

Qy    305 GCCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTCTGGC 364
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Db    301 GCCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTCTGGC 360

Qy    365 CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAA 424
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Db    361 CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAA 420

Qy    425 AGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAG 484
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAG 480

Qy    485 ATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT 544

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Db	481		ATGGAAACCCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	540
Qy	545		GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCACCTTTT	604
Db	541		GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCACCTTTT	600
Qy	605		CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	664
Db	601		CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	660
Qy	665		AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAA	724
Db	661		AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAA	720
Qy	725		TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGCAACT	784
Db	721		TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGCAACT	780
Qy	785		CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGTGATAGCC	844
Db	781		CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGTGATAGCC	840
Qy	845		AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	841		AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	900
Qy	905		CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	901		CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	960
Qy	965		TTCCCCCTTTTTCAGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	961		TTCCCCCTTTTTCAGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1020
Qy	1025		GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGGAATTGGGATTCCTTTG	1084
Db	1021		GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGGAATTGGGATTCCTTTG	1080
Qy	1085		GTAACCTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCTTGAA	1144
Db	1081		GTAACCTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCTTGAA	1140
Qy	1145		GCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1204
Db	1141		GCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1200
Qy	1205		CTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	1201		CTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1260
Qy	1265		GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1324
Db	1261		GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1320
Qy	1325		GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384

Db	1321	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1380
Qy	1385	CGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTGGTTC	1444
Db	1381	CGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTGGTTC	1440
Qy	1445	CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTATAACGAAATGGACAAGAACCGA	1504
Db	1441	CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTATAACGAAATGGACAAGAACCGA	1500
Qy	1505	TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG	1564
Db	1501	TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG	1560
Qy	1565	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1624
Db	1561	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1620
Qy	1625	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1684
Db	1621	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1680
Qy	1685	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1744
Db	1681	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1740
Qy	1745	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAATC	1804
Db	1741	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAATC	1800
Qy	1805	CTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1864
Db	1801	CTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1860
Qy	1865	TTCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1924
Db	1861	TTCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1920
Qy	1925	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1984
Db	1921	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1980
Qy	1985	GCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2044
Db	1981	GCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2040
Qy	2045	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2104
Db	2041	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2100
Qy	2105	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGAT	2164
Db	2101	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGAT	2160
Qy	2165	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2224
Db	2161	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2220

Qy	2225	GGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2284
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Qy	2285	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAAATA	2344
Db	2281	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAAATA	2340
Qy	2345	GTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTAAACAC	2404
Db	2341	GTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTAAACAC	2400
Qy	2405	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2464
Db	2401	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2460
Qy	2465	GCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2524
Db	2461	GCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2520
Qy	2525	TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTCA	2584
Db	2521	TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTCA	2580
Qy	2585	ATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAAA	2644
Db	2581	ATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAAA	2640
Qy	2645	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCAG	2704
Db	2641	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCAG	2700
Qy	2705	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2764
Db	2701	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2760
Qy	2765	TTCGGAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2824
Db	2761	TTCGGAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2820
Qy	2825	TCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2884
Db	2821	TCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2880
Qy	2885	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2944
Db	2881	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2940
Qy	2945	AATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTTTTCAG	3004
Db	2941	AATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTTTTCAG	3000
Qy	3005	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCACCATTTCAAAGGGCC	3064
Db	3001	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCACCATTTCAAAGGGCC	3060

Qy	3065	CACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3124
Db	3061	CACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3120
Qy	3125	TCTTTTACTAGTGTGTGTGTATATATAAACAATTGTAAATTTCTTTTAGCCCATTT	3184
Db	3121	TCTTTTACTAGTGTGTGTGTATATATAAACAATTGTAAATTTCTTTTAGCCCATTT	3180
Qy	3185	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3244
Db	3181	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3240
Qy	3245	TGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCT	3304
Db	3241	TGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCT	3300
Qy	3305	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3364
Db	3301	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3360
Qy	3365	GCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3424
Db	3361	GCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3420
Qy	3425	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3484
Db	3421	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3480
Qy	3485	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3544
Db	3481	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3540
Qy	3545	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3604
Db	3541	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3600
Qy	3605	TGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3664
Db	3601	TGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3660
Qy	3665	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3724
Db	3661	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3720
Qy	3725	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3784
Db	3721	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3780
Qy	3785	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3844
Db	3781	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3840
Qy	3845	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATTC	3904
Db	3841	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATTC	3900
Qy	3905	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3964



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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3901 AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC 3960
Qy      3965 TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA 4024
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3961 TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA 4020
Qy      4025 ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA 4083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA 4079

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RESULT 3

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US-09-175-658B-20
; Sequence 20, Application US/09175658B
; Patent No. 6372900
; GENERAL INFORMATION:
; APPLICANT: METALLINOS, DANIKA
; APPLICANT: RINE, JASPER
; APPLICANT: BOWLING, ANN
; TITLE OF INVENTION: HORSE ENDOTHELIN-B RECEPTOR GENE AND GENE PRODUCTS
; FILE REFERENCE: GOBR-110
; CURRENT APPLICATION NUMBER: US/09/175,658B
; CURRENT FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/062,562
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Horse
US-09-175-658B-20

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Query Match          9.9%; Score 406.2; DB 4; Length 1321;
Best Local Similarity 67.2%; Pred. No. 1.2e-96;
Matches 630; Conservative 0; Mismatches 283; Indels 24; Gaps 3;

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Qy      717 CTTTCAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGA 776
          ||||||| ||||| ||||| || | || || | ||| | ||| || | || |
Db      310 CTTTCAAGTACATCAACACAGTAGTGTCTGCCTAGTGTTCTGCTGGGCATCATCGGAA 369
Qy      777 ATGCAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGC 836
          | | || ||||| || |||||||| ||||||| || || ||| ||||| ||
Db      370 ACTCCACACTGCTGAGAATCATTTACAAGAACAAGTGCATGCGGAACGGCCCTAATATCT 429
Qy      837 TGATAGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATG 896
          ||||| ||||| || || || ||||||| | | | ||||||| ||| |||||||
Db      430 TGATCGCCAGCCTGGCTCTCCGAGACCTGCTGCAAATCATCATTTGACGTCCCCATCAATG 489
Qy      897 TATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTT 956
          | | |||||||||||| | ||||| ||||||| || | |
Db      490 TCTACAAGCTGCTGGCTGAGGACTGGCC-----CTTTGGAGTCGAGATGT 534
Qy      957 GCAAGCTGTTCCCTTTTTCAGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCG 1016
          | ||||| | || || | |||||| |||| ||||| |||| | || | || || |
Db      535 GTAAGCTGGTGCCTTTCATACAGAAGGCCCTCCGTGGGCATCACTGTGCTGAGTCTGTGTG 594

```



```

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1203:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1470 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g182275
US-09-016-434-1203

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Query Match          9.6%; Score 395.8; DB 4; Length 1470;
Best Local Similarity 65.7%; Pred. No. 6.7e-94;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

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Qy      689 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748
        |||| |  |  |  | || |  ||||| ||||| || | || |
Db      314 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCTGC 373

Qy      749 ACTATTTTCATCGTGGGAATGGTGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808
        | | || |  |||| ||  | |||| | || | || | || | || | || |
Db      374 CTTGTGTTTCGTGCTGGGGATCATCGGGAAGTCCACACTTCTGAGAATTATCTACAAGAAC 433

Qy      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC 868
        || || || |  || || |||| | || |||| | || | ||||| |
Db      434 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 493

Qy      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928
        |  | ||||| || ||||| ||||| | ||||| || | |||||
Db      494 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 549

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Qy 929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTGCAGAAGTCCTCG 988  
 ||||| | | | | | | | | | | | | | | | | | |  
 Db 550 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC 598  
 Qy 989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1048  
 ||||| ||||| || || | | || || ||||| || | ||||| || || ||||| |||||  
 Db 599 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 658  
 Qy 1049 TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCC 1108  
 || ||||| | | | | ||||| |||| | | | | | | ||||| |  
 Db 659 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 718  
 Qy 1109 ATCTGGATCCTGTCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATGGTACCC 1168  
 || ||| | | || | | |||| | ||||| || || || | | | |  
 Db 719 ATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 778  
 Qy 1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 779 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAGAAGACAGCT 838  
 Qy 1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1282  
 ||||| |||| ||| | | ||| || ||||| || | ||||| ||||| ||  
 Db 839 TTCATGCAGTTTACAAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTG 898  
 Qy 1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342  
 || |||| | |||| | || || || || || || || || || || || || ||  
 Db 899 CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG 955  
 Qy 1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402  
 || | || || || || || | | || || || || || || || || || || || || ||  
 Db 956 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1015  
 Qy 1403 ACAGTTTTCTGCTTGCTTGTAAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT 1462  
 || || || || || || | | |||| || ||||| | || ||||| | ||| |  
 Db 1016 ACCGTCTTTTGCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTCAGCAGG 1075  
 Qy 1463 ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522  
 || |||| | || | |||| | | || || || ||||| | | || ||  
 Db 1076 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTTT 1135  
 Qy 1523 TTAAGTCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC 1582  
 | || | |||| || || |||| || || || | ||||| || || |||||  
 Db 1136 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1195  
 Qy 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTTGTTTCCAGTCATGCCTCTGCTGC 1642  
 || ||||| ||||| ||||| || || |||| || || ||||| || |||||  
 Db 1196 ATTGCTCTGTATTTGGTGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC 1255  
 Qy 1643 TGCTG 1647  
 || ||  
 Db 1256 TGGTG 1260

RESULT 5  
 US-08-910-864-13  
 ; Sequence 13, Application US/08910864  
 ; Patent No. 6280931



Qy 809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC 868  
 || || ||| | || || |||| | ||| |||| | || || ||||| |  
 Db 618 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 677

Qy 869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928  
 | | ||||| | ||||| |||| | ||||| | | |||||  
 Db 678 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 733

Qy 929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGT'TCCCCTTTTTGCAGAAGTCCTCG 988  
 |||| | | |||| | || | |||| ||||  
 Db 734 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAAGCCTCC 782

Qy 989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGCAGTTGCC 1048  
 |||| |||| | || | || | |||| | ||||| || |||| |||||  
 Db 783 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 842

Qy 1049 TCCTGGAGTCGTGTTTTCAGGGAATTGGGATTCCCTTTGGTAAGTACCATTGAAATTGTCTCC 1108  
 || ||||| | || | ||||| |||| | || | ||||| |  
 Db 843 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 902

Qy 1109 ATCTGGATCCTGTCTTTTATCCTGGCCATTCCCTGAAGCGATTGGCTTCGTCATGGTACCC 1168  
 || || | | || | | |||| | ||||| || || | | || |  
 Db 903 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 962

Qy 1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222  
 | || || | || | | || || || || || || | ||  
 Db 963 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCCTTCAGAAGACAGCT 1022

Qy 1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTCTATTTCTGTATG 1282  
 ||||| |||| ||| | | || | ||||| || | ||||| ||  
 Db 1023 TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTATTCAGTTTCTATTTCTGCTTG 1082

Qy 1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342  
 || |||| | |||| | || | || || |||| |||| |||| | ||| |  
 Db 1083 CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG 1139

Qy 1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402  
 || | || || |||| | | || | || |||| | || ||||| |||  
 Db 1140 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1199

Qy 1403 ACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT 1462  
 || || || ||| |||| | | |||| | ||||| | || ||||| | ||| |  
 Db 1200 ACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACTCAGCAGG 1259

Qy 1463 ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522  
 || |||| | || | |||| | | || | || ||||| | || ||||  
 Db 1260 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAAC'TTTTGAGCTTT 1319

Qy 1523 TTAAGTCTCATGGATTACATCGGTATTAACCTTGGCAACCATGAATTCATGTATAAACCCC 1582  
 | || | |||| || || |||| || |||| | ||||| || || |||||  
 Db 1320 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1379

Qy 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642  
 || ||||| |||| | || |||| | || ||||| | |||||  
 Db 1380 ATTGCTCTGTATTTGGTGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC 1439

Qy 1643 TGCTG 1647

Db            11 11  
             1440 TGGTG 1444

RESULT 6

US-08-121-446-3

; Sequence 3, Application US/08121446  
; Patent No. 6313276  
; GENERAL INFORMATION:  
; APPLICANT: IMURA, HIROO  
; APPLICANT: NAKAO, KAZUWA  
; APPLICANT: NAKANISHI, SHIGETADA  
; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/121,446  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/911,684  
; FILING DATE: 10-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CIOTTI, THOMAS E.  
; REGISTRATION NUMBER: 21,013  
; REFERENCE/DOCKET NUMBER: 29900-20324.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4301 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 238..1566  
US-08-121-446-3

Query Match                    9.6%;   Score 395.8;   DB 4;   Length 4301;  
Best Local Similarity       65.7%;   Pred. No. 1.2e-93;  
Matches 634; Conservative       0; Mismatches 307; Indels    24; Gaps       3;

Qy                    689 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748

Db	505	TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCTGC	564
Qy	749	ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC	808
Db	565	CTTGTGTTTCGTGCTGGGGATCATCGGGAACCCACACTTCTGAGAATTATCTACAAGAAC	624
Qy	809	AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC	868
Db	625	AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG	684
Qy	869	TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT	928
Db	685	CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----	740
Qy	929	GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTCGAGAAGTCCTCG	988
Db	741	-----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAAGCCTCC	789
Qy	989	GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC	1048
Db	790	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	849
Qy	1049	TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCCTTTGGTAACTGCCATTGAAATTGTCTCC	1108
Db	850	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAAATTGTTTTG	909
Qy	1109	ATCTGGATCCTGTCCTTTATCCTGGCCATTCCCTGAAGCGATTGGCTTCGTCATGGTACCC	1168
Db	910	ATTTGGGTGGTCTCTGTGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	969
Qy	1169	TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA	1222
Db	970	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCCTTCAGAAGACAGCT	1029
Qy	1223	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTCTATTTCTGTATG	1282
Db	1030	TTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTG	1089
Qy	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
Db	1090	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG	1146
Qy	1343	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Db	1147	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA	1206
Qy	1403	ACAGTTTTTCTGCTTGTTGTAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT	1462
Db	1207	ACCGTCTTTTGCTGGTCCCTTGCTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGG	1266
Qy	1463	ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1267	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTTT	1326
Qy	1523	TTACTGCTCATGGATTACATCGGTATTAACTTGGCAACCATGAATTCATGTATAAACCCC	1582



Db 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386

Qy 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642  
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1387 ATTGCTCTGTATTTGGTGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGC 1446

Qy 1643 TGCTG 1647  
 || ||

Db 1447 TGGTG 1451

RESULT 7

PCT-US92-02091-1

; Sequence 1, Application PC/TUS9202091

; GENERAL INFORMATION:

; APPLICANT: Battey Jr., James F.

; APPLICANT: Corjay, Martha H.

; APPLICANT: Feldman, Richard I.

; APPLICANT: Harkins, Richard N.

; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwin P. Ching

; STREET: 1501 Harbor Bay Parkway

; CITY: Alameda

; STATE: CA

; COUNTRY: USA

; ZIP: 94501

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/02091

; FILING DATE: 19920313

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/426,150

; FILING DATE: 24-OCT-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/533,659

; FILING DATE: 05-JUN-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34090

; REFERENCE/DOCKET NUMBER: A-0092C

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-266-7476

; TELEFAX: 415-266-7400

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1700 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; CELL LINE: Swiss 3T3
; IMMEDIATE SOURCE:
; LIBRARY: Lambda GT10
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 378..1532
PCT-US92-02091-1
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Query Match          2.5%; Score 101.8; DB 5; Length 1700;
Best Local Similarity 49.3%; Pred. No. 1.4e-16;
Matches 308; Conservative 0; Mismatches 302; Indels 15; Gaps 1;
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Qy      714 CAGCTTTCAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGG 773
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      490 CGGGCTTCATCTATGTCATCCCTGCAGTTTATGGGCTTATCATCGTGATAGGTCTTATTG 549

Qy      774 GGAATGCAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACG 833
      | | | | | | | | | | | | | | | | | | | | | |
Db      550 GCAACATCACGCTCATCAAGATCTTCTGCACGGTCAAGTCCATGCGAAACGTGCCAAACC 609

Qy      834 CGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCA 893
      | | | | | | | | | | | | | | | | | | | | | |
Db      610 TGTTTCATCTCTAGCCTGGCTTTGGGAGACCTGCTGCTGCTGGTGACATGCGCCCTGTGG 669

Qy      894 ATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTTC 953
      | | | | | | | | | | | | | | | | | | | | | |
Db      670 ATGCCAGCAAGTACCTGGCTGACAGGTGGCTA-----TTTGGCAGAATTG 714

Qy      954 TTTGCAAGCTGTTCCCTTTTTCGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCT 1013
      | | | | | | | | | | | | | | | | | | | | | |
Db      715 GCTGCAAACTGATCCCTTTTATACAACTTACTTCAGTGGGGGTGTCTGTCTTCACACTTA 774

Qy      1014 GCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTG 1073
      | | | | | | | | | | | | | | | | | | | | | |
Db      775 CGGCACTGTCAGCTGACAGGTACAAAGCCATTGTACGGCCAATGGATATCCAGGCATCCC 834

Qy      1074 GGATTCCCTTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGG 1133
      | | | | | | | | | | | | | | | | | | | | | |
Db      835 ATGCCCTGATGAAGATCTGTCTCAAAGCTGCTTTGATCTGGATTGTCTCTATGTTGTTGG 894

Qy      1134 CCATTCCCTGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATA 1193
      | | | | | | | | | | | | | | | | | | | | | |
Db      895 CCATCCCAGAGGCTGTGTTTCTGACCTCCACCCCTTCATGTGAAAGATACCAACCAAAA 954

Qy      1194 AAACCTGTATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACT 1253
      | | | | | | | | | | | | | | | | | | | | | |
Db      955 CCTTCATTAGTTGTGCCCCCTACCCACACTCCAATGAGCTACACCCTAAAATCCATTCCA 1014

Qy      1254 GGTGGCTCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCC 1313
      | | | | | | | | | | | | | | | | | | | | | |
Db      1015 TGGCTTCCTTTCTGGTCTTCTACGTTATCCCACTGGCGATCATCTCTGTCTACTACTACT 1074

Qy      1314 TCATGACTTGTGAGATGTTGAACAG 1338
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Db      514 TCCTCTATGTCATCCCTGCAGTTTATGGGGTTATCATTCTGATAGGCCCTCATTGGCAACA 573
Qy      780 CAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGA 839
      ||| || ||| |||| | |      ||| | ||| | || | || ||| | | |
Db      574 TCACTTTGATCAAGATCTTCTGTACAGTCAAGTCCATGCGAAACGTTCCAAACCTGTTCA 633
Qy      840 TAGCCAGTCTTGCCCTTGGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTAT 899
      | ||||| || | ||||| || | | | | | || | |||
Db      634 TTTCCAGTCTGGCTTTGGGAGACCTGCTCCTCTAATAACGTGTGCTCCAGTGGATGCCA 693
Qy      900 TTAAGCTGCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCA 959
      | | ||||| | ||| ||| | || | |||
Db      694 GCAGGTACCTGGCTGACAGATGGCTATTTGGCAGGATTGGC-----TGCA 738
Qy      960 AGCTGTTCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTC 1019
      | ||| ||||| | || | ||| | || | ||| ||| |||
Db      739 AACTGATCCCCTTTATACAGCTTACCTCTGTTGGGGTGTCTGTCTTCACACTCACGGCGC 798
Qy      1020 TTAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTC 1079
      | | | |||| ||| || | || | | | ||| |
Db      799 TCTCGGCAGACAGATACAAAGCCATTGTCCGGCCAATGGATATCCAGGCCTCCCATGCCC 858
Qy      1080 CTTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCTGGCCATTC 1139
      || | | | || | || | ||| ||| | ||| |||||
Db      859 TGATGAAGATCTGCCTCAAAGCCGCCTTTATCTGGATCATCTCCATGCTGCTGGCCATTC 918
Qy      1140 CTGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCT 1199
      | ||| | | | | ||| | | | | ||| | |
Db      919 CAGAGGCCGTGTTTTCTGACCTCCATCCCTTCCATGAGGAAAGCACCAACCAGACCTTCA 978
Qy      1200 GTATGCTCAATGCCACATCAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGC 1259
      || | | | || | | ||| ||| | | | | |
Db      979 TTAGCTGTGCCCCATACCCACACTCTAATGAGCTTCACCCCAAATCCATTCTATGGCTT 1038
Qy      1260 TCTTCGGGTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGA 1319
      ||| | ||| | | ||| || | || | | ||| | |||
Db      1039 CCTTTCTGGTCTTCTACGTCATCCCACTGTCGATCATCTCTGTTTACTACTACTTCATTG 1098
Qy      1320 CTTGTGAGATGTTGAACAG 1338
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Db      1099 CTAAAAATCTGATCCAGAG 1117

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RESULT 9

PCT-US92-02091-3

; Sequence 3, Application PC/TUS9202091

; GENERAL INFORMATION:

; APPLICANT: Battey Jr., James F.

; APPLICANT: Corjay, Martha H.

; APPLICANT: Feldman, Richard I.

; APPLICANT: Harkins, Richard N.

; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwin P. Ching

; STREET: 1501 Harbor Bay Parkway

; CITY: Alameda

```

; STATE: CA
; COUNTRY: USA
; ZIP: 94501
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02091
; FILING DATE: 19920313
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/426,150
; FILING DATE: 24-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/533,659
; FILING DATE: 05-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34090
; REFERENCE/DOCKET NUMBER: A-0092C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-266-7476
; TELEFAX: 415-266-7400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1726 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: Small cell lung carcinoma
; CELL LINE: NCI-H345
; IMMEDIATE SOURCE:
; LIBRARY: Lambda GT10
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 399..1553
PCT-US92-02091-3

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Query Match          2.2%; Score 91; DB 5; Length 1726;
Best Local Similarity 48.3%; Pred. No. 9.9e-14;
Matches 299; Conservative 0; Mismatches 305; Indels 15; Gaps 1;

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Qy      720 TCAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATG 779
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Db      514 TCCTCTATGTCATCCCTGCAGTTTATGGGGTTATCATTCTGATAGGCCTCATGGCAACA 573

Qy      780 CAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGA 839
          ||| || ||| ||| ||  ||  ||| ||  ||| ||  ||| ||  |||
Db      574 TCACTTTGATCAAGATCTTCTGTACAGTCAAGTCCATGCGAAACGTTCCAAACCTGTTCA 633

Qy      840 TAGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTAT 899

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Db      634 TTTCCAGTCTGGCTTTGGGAGACCTGCTCCTCCTAATAACGTGTGCTCCAGTGGATGCCA 693
Qy      900 TTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCA 959
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      694 GCAGGTACCTGGCTGACAGATGGCTATTTGGCAGGATTGGC-----TGCA 738
Qy      960 AGCTGTTCCCTTTTTGCGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTC 1019
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      739 AACTGATCCCCTTTATACAGCTTACCTCTGTTGGGGTGTCTGTCTTCACACTCACGGCGC 798
Qy      1020 TTAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGAATTGGGATTC 1079
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      799 TCTCGGCAGACAGATACAAAGCCATTGTCCGGCCAATGGATATCCAGGCCCTCCCATGCCC 858
Qy      1080 CTTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTC 1139
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      859 TGATGAAGATCTGCCTCAAAGCCGCCTTTATCTGGATCATCTCCATGCTGCTGGCCATTC 918
Qy      1140 CTGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCT 1199
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      919 CAGAGGCCGTGTTTTCTGACCTCCATCCCTTCCATGAGGAAAGCACCAACCAGACCTTCA 978
Qy      1200 GTATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGC 1259
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      979 TTAGCTGTGCCCCATACCCACACTCTAATGAGCTTCACCCCAAATCCATTCTATGGCTT 1038
Qy      1260 TCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGA 1319
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1039 CCTTTCTGGTCTTCTACGTCATCCACTGTGATCATCTCTGTTTACTACTACTTCATTG 1098
Qy      1320 CTTGTGAGATGTTGAACAG 1338
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1099 CTAAAAATCTGATCCAGAG 1117

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RESULT 10

US-09-120-772-1

; Sequence 1, Application US/09120772

; Patent No. 6143521

; GENERAL INFORMATION:

; APPLICANT: LANE, PAMELA

; APPLICANT: TSUI, PING

; APPLICANT: ELSHOURBAGY, NABIL

; TITLE OF INVENTION: HUMAN BOMBESIN RECEPTOR SUBTYPE

; TITLE OF INVENTION: 3

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ratner & Prestia

; STREET: P.O. Box 980

; CITY: Valley Forge

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

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;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/120,772
;   FILING DATE:  22-JUL-1998
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Prestia, Paul F
;   REGISTRATION NUMBER:  23,031
;   REFERENCE/DOCKET NUMBER:  GP-70505
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  610-407-0700
;   TELEFAX:  610-407-0700
;   TELEX:  846169
;   INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1205 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
US-09-120-772-1

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Query Match          1.9%;  Score 79.6;  DB 3;  Length 1205;
Best Local Similarity  46.9%;  Pred. No. 8.1e-11;
Matches 419;  Conservative  0;  Mismatches 439;  Indels  36;  Gaps  4;

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Qy      761 GTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGG 820
        ||||| || | || ||||| | || | || || | || ||||| |||
Db      180 GTGGGCATCCTTGGAATGCTATTCTCATCAAAGTCTTTTCAAGACCAAATCCATGCAA 239

Qy      821 AATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATT 880
        | | || || | || |||| | || ||||| ||| | | || | | |
Db      240 ACAGTTCCAAATATTTTCATCACCAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACT 299

Qy      881 GATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGAC 940
        | ||| | ||| | | | |||| | | |||| ||
Db      300 TGTGTGCCAGTGGATGCAACTCACTACCTTGCAAGGATGGCTGTTC----- 347

Qy      941 TTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACC 1000
        || | || |||| || || || || | || | || || || | |
Db      348 ---GGAAGAATTGGTTGTAAGGTGCTCTCTTTCATCCGGCTCACTTCTGTTGGTGTGTCA 404

Qy     1001 GTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGT 1060
        || ||| | |||| || | ||||| |||| | ||||| |
Db      405 GTGTTACATTAGCAATTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAG 464

Qy     1061 GTTCAGGGAATTGGGATTCCCTTTGGTAAGTCCATTGAAATTGTCTCCATCTGGATCCTG 1120
        ||| || || || | || || || || | ||||| ||
Db      465 CGACAGCCCTCCAATGCCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCGTG 524

Qy     1121 TCCTTTATCCTGGCCATTCCCTGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGG 1180
        || | || | || | |||| || || | | | |||| | ||
Db      525 TCTATGATATTTGCTCTACCTGAGGCTATATTTTCAAATGTATACACTTTTCGAGATCCC 584

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Qy 1181 GGTGAACAGCATAAAACCTGTATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAA 1240  
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 Db 585 AATAAAAATATGACATTTGAATCATGTACCTCTTATCCTGTCTCTAAGAAGCTCTTGCAA 644  
 Qy 1241 GATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCG 1300  
 | | | | | | | | | | | | | | | | | |  
 Db 645 GAAATACATTCTCTGCTGTGCTTCTTAGTGTTCTACATTATTCCACTCTCTATTATCTCT 704  
 Qy 1301 ATCTTCTACACCTCATGACTTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATT 1360  
 | | | | | | | | | | | | | | | | | |  
 Db 705 GTCTACTATTCTTGATTGCTAGGACCCCTTACAAAAGCACCTGAACATACCTACTGAG 764  
 Qy 1361 GCCCTCAGTGAACATCTTAAGCAG-----CGTCGAGAAGTGGCAAAAACAGTTTTC 1411  
 | | | | | | | | | | | | | | | | | |  
 Db 765 GAACAAAGCCATGCCCGTAAGCAGATTGAATCCCGAAAGAGAATTGCCAGAACGGTATTG 824  
 Qy 1412 TGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTCTTCACTTAAGCCGTATATTGAAG 1471  
 | | | | | | | | | | | | | | | | | |  
 Db 825 GTGTTGGTGGCTCTGTTTGGCCCTCTGCTGGTTGCCAAATCACCT--CCTGTACCTCTACC 882  
 Qy 1472 AAAACTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTCTTACTGCTC 1531  
 | | | | | | | | | | | | | | | | | |  
 Db 883 ATTCATTCACTTCTCAAACCTATGTAGACCCCTCTGCCATGCATTTCAATTTTACCATT- 941  
 Qy 1532 ATGGATTACATCGGTATTAAGTGGCAACCATGAATTCATGTATAAACCCCATAGCTCTG 1591  
 | | | | | | | | | | | | | | | | | |  
 Db 942 -----TTCTCTCGGGTTTTGGCTTTCAGCAATTCTTGCGTAAACCCCTTGTCTC 992  
 Qy 1592 TATTTTGTGAGCAAGAAATTTAAAATTTGTTTCCAGTCATGCCTCTGCTGCTGC 1645  
 | | | | | | | | | | | | | | | | | |  
 Db 993 TACTGGCTGAGCAAAAGCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTGTTGC 1046

RESULT 11

US-09-016-434-1275

; Sequence 1275, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:



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; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1275:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g291876
US-09-016-434-1275

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Query Match          1.9%; Score 79.6; DB 4; Length 1413;
Best Local Similarity 46.9%; Pred. No. 8.8e-11;
Matches 419; Conservative 0; Mismatches 439; Indels 36; Gaps 4;

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Qy      761 GTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGG 820
        ||||| || | || ||||| | || | || | ||| ||||| |||
Db      327 GTGGGCATCCTTGGAATGCTATTCTCATCAAAGTCTTTTCAAGACCAAATCCATGCAA 386

Qy      821 AATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATT 880
        | | || || | || |||| | || ||||| ||| | | || | |
Db      387 ACAGTTCCAAATATTTTCATCACCAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACT 446

Qy      881 GATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGAC 940
        | ||| | ||| | | | || || | |||| ||
Db      447 TGTGTGCCAGTGGATGCAACTCACTACCTTGCAAGGATGGCTGTTC----- 494

Qy      941 TTTGGCGTATTTCTTTGCAAGCTGTTCCTTTTGCAGAAGTCCTCGGTGGGGATCACC 1000
        || | || |||| || || || || || | || || || | |
Db      495 ---GGAAGAATTGGTTGTAAGGTGCTCTTTTCATCCGGCTCACTTCTGTTGGTGTGTCA 551

Qy      1001 GTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGT 1060
        || ||| | |||| || ||||| |||| ||||| |
Db      552 GTGTTACATTAACAATTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAG 611

Qy      1061 GTTCAGGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTG 1120
        ||| || || || | || || || || || || || || ||
Db      612 CGACAGCCCTCCAATGCCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCGTG 671

Qy      1121 TCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGG 1180
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Db      672 TCTATGATATTTGCTCTACCTGAGGCTATATTTTCAAATGTATACACTTTTCGAGATCCC 731

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Qy 1181 GGTGAACAGCATATAAACCTGTATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAA 1240  
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 Db 732 AATAAAAATATGACATTTGAATCATGTACCTCTTATCCTGTCTCTAAGAAGCTCTTGCAA 791  
 Qy 1241 GATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCG 1300  
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 Db 792 GAAATACATTCTCTGCTGTGCTTCTTAGTGTTCTACATTATTCACCTCTCTATTATCTCT 851  
 Qy 1301 ATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATT 1360  
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 Db 852 GTCTACTATTCTTGATTGCTAGGACCCTTTACAAAAGCACCTGAACATACCTACTGAG 911  
 Qy 1361 GCCCTCAGTGAACATCTTAAGCAG-----CGTCGAGAAGTGGCAAAAACAGTTTTC 1411  
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 Db 912 GAACAAAGCCATGCCCGTAAGCAGATTGAATCCCGAAAGAGAATTGCCAGAACGGTATTG 971  
 Qy 1412 TGCTTGTTGTAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGTATATTGAAG 1471  
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 Db 972 GTGTTGGTGGCTCTGTTTGGCCTCTGCTGGTTGCCAAATCACCT--CCTGTACCTCTACC 1029  
 Qy 1472 AAAACTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTCTTACTGCTC 1531  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1030 ATTCATTCACTTCTCAAACCTATGTAGACCCCTCTGCCATGCATTTTCACTTTTACCATT- 1088  
 Qy 1532 ATGGATTACATCGGTATTAACCTTGGCAACCATGAATTCATGTATAAACCCCATAGCTCTG 1591  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1089 -----TTCTCTCGGGTTTTGGCTTTTCAGCAATTCTTGCGTAAACCCCTTTGCTCTC 1139  
 Qy 1592 TATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGCTGC 1645  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1140 TACTGGCTGAGCAAAAGCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTGTTGC 1193

RESULT 12

US-09-016-434-1233

; Sequence 1233, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

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; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1233:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1352 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g189241
US-09-016-434-1233

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Query Match          1.7%; Score 68.6; DB 4; Length 1352;
Best Local Similarity 50.1%; Pred. No. 6.7e-08;
Matches 210; Conservative 0; Mismatches 194; Indels 15; Gaps 1;

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Qy      752 ATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAACAAA 811
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Db      296 ATCATCACCGTGGGCTTGCTGGGCAACATCATGCTGGTGAAGATCTTCATCACCAACAGC 355

Qy      812 TGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATCTAT 871
      ||||| || ||||| || || | | || || || ||| | |
Db      356 GCCATGAGGAGCGTCCCCAACATCTTCATCTCTAACCTGGCGGCCGGGGACTTGCTGCTG 415

Qy      872 GTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGAT 931
      || ||| |||| | || | | |||| || ||
Db      416 CTGCTCACCTGCGTCCC-----GGTGGACGCCTCGCGCTACTTCTTCGCAC 460

Qy      932 CACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTGCAGAAGTCCTCGGTG 991
      | ||||| | |||| ||| ||| | | ||| | || |||
Db      461 GAGTGGATGTTTGGCAAGGTGGGCTGCAAAGTATCCCTGTCATCCAGCTCACTTCCGTG 520

Qy      992 GGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCCTCC 1051
      ||| | |||| ||| || || || || | ||||| ||||| | | |
Db      521 GGGGTTTCCGTGTTCACTCTCACTGCCCTCAGCGCCGACAGGTACAGAGCCATCGTTAAC 580

Qy      1052 TGGAGTCGTGTTCAAGGAATTGGGATTCCCTTTGGTAAGTCCCATTTGAAATTGTCTCCATC 1111
      | | ||| ||| || || | | | | |||
Db      581 CCCATGGACATGCAGACGTGAGGGGCATTGCTGCGGACCTGTGTGAAGGCCATGGGTATC 640

Qy      1112 TGGATCCTGTCCTTTATCCTGGCCATTCCCTGAAGCGATTGGCTTCGTCATGGTACCCTT 1170
      ||| | | ||| | | |||| |||| ||||| | | | ||| |||
Db      641 TGGGTGGTCTCCGTGTTGCTGGCAGTTCCCGAAGCGGTGTTTTCAGAAGTGGCTCGCAT 699

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RESULT 13  
 PCT-US92-02091-7  
 ; Sequence 7, Application PC/TUS9202091  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Battey Jr., James F.  
 ; APPLICANT: Corjay, Martha H.  
 ; APPLICANT: Feldman, Richard I.  
 ; APPLICANT: Harkins, Richard N.  
 ; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Edwin P. Ching  
 ; STREET: 1501 Harbor Bay Parkway  
 ; CITY: Alameda  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94501  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US92/02091  
 ; FILING DATE: 19920313  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/426,150  
 ; FILING DATE: 24-OCT-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/533,659  
 ; FILING DATE: 05-JUN-1990  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ching, Edwin P.  
 ; REGISTRATION NUMBER: 34090  
 ; REFERENCE/DOCKET NUMBER: A-0092C  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-266-7476  
 ; TELEFAX: 415-266-7400  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1352 base pairs  
 ; TYPE: NUCLEIC ACID  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; HYPOTHETICAL: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; CELL TYPE: Small cell lung carcinoma  
 ; CELL LINE: NCI-H345  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 140..1312  
 PCT-US92-02091-7

Query Match

1.7%; Score 68.6; DB 5; Length 1352;

Best Local Similarity 50.1%; Pred. No. 6.7e-08;  
Matches 210; Conservative 0; Mismatches 194; Indels 15; Gaps 1;

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Qy      752 ATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAACAAA 811
      || ||| ||||| || |||| | | || | | |||| | | |||
Db      296 ATCATCACCGTGGGCTTGCTGGGCAACATCATGCTGGTGAAGATCTTCATCACCAACAGC 355

Qy      812 TGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATCTAT 871
      ||||| | ||||| | || | | || | | || ||| | |
Db      356 GCCATGAGGAGCGTCCCCAACATCTTCATCTCTAACCTGGCGGCCGGGACTTGCTGCTG 415

Qy      872 GTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGAT 931
      || ||| |||| | || | | |||| | || |
Db      416 CTGCTCACCTGCGTCCC-----GGTGGACGCCTCGCGCTACTTCTTCGAC 460

Qy      932 CACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTCGAGAAGTCCTCGGTG 991
      | ||||| | |||| ||| ||| | | || | || |||
Db      461 GAGTGGATGTTTGGCAAGGTGGGCTGCAAACTGATCCCTGTCATCCAGCTCACTTCCGTG 520

Qy      992 GGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCCTCC 1051
      ||| | |||| ||| ||| || || | | ||||| ||| | |
Db      521 GGGGTTTCCGTGTTCACTCTCACTGCCCTCAGCGCCGACAGGTACAGAGCCATCGTTAAC 580

Qy      1052 TGGAGTCGTGTTCAGGGAATTGGGATTCTTTGGTAAGTCCATTGAAATTGTCTCCATC 1111
      | | ||| ||| || || | | | | |||
Db      581 CCCATGGACATGCAGACGTGAGGGGCATTGCTGCGGACCTGTGTGAAGGCCATGGGTATC 640

Qy      1112 TGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATGGTACCCTT 1170
      ||| | | ||| | | |||| |||| |||| | | ||| |||
Db      641 TGGGTGGTCTCCGTGTTGCTGGCAGTTCCCGAAGCGGTGTTTTTCAGAAGTGGCTCGCAT 699

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# RESULT 14

PCT-US92-02091-5

; Sequence 5, Application PC/TUS9202091

## ; GENERAL INFORMATION:

; APPLICANT: Battey Jr., James F.

; APPLICANT: Corjay, Martha H.

; APPLICANT: Feldman, Richard I.

; APPLICANT: Harkins, Richard N.

; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwin P. Ching

; STREET: 1501 Harbor Bay Parkway

; CITY: Alameda

; STATE: CA

; COUNTRY: USA

; ZIP: 94501

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/02091

; FILING DATE: 19920313

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/426,150
; FILING DATE: 24-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/533,659
; FILING DATE: 05-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34090
; REFERENCE/DOCKET NUMBER: A-0092C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-266-7476
; TELEFAX: 415-266-7400
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1584 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus rattus
; TISSUE TYPE: Esophagus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 132..1304
PCT-US92-02091-5

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Query Match          1.6%; Score 65.8; DB 5; Length 1584;
Best Local Similarity 49.6%; Pred. No. 4e-07;
Matches 209; Conservative 0; Mismatches 197; Indels 15; Gaps 1;

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Qy      752 ATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAACAAA 811
      || || |||| || |||| || | ||| | | || | | |||
Db      288 ATCATCTCGGTGGGCTTGCTGGGCAACATCATGCTGGTGAAGATATTCCTCACCAACAGC 347

Qy      812 TGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATCTAT 871
      ||| ||| || ||||| | || | | || || ||||| |
Db      348 ACCATGCGGAGTGTCCCCAACATCTTCATCTCTAACCTGGCTGCGGGAGACCTGCTGCTG 407

Qy      872 GTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGAT 931
      || | | |||| | || | | || | |||||
Db      408 CTGCTGACCTGCGTCCCAGTGGATGCCTCC-----CGATACTTCTTTGAT 452

Qy      932 CACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTGCAGAAGTCCTCGGTG 991
      | | | ||| | |||| || ||| | ||| |||||
Db      453 GAATGGGTGTTTCGGCAAGCTGGGCTGCAAACTCATCCAGCCATCCAGCTCACCTCGGTG 512

Qy      992 GGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCCTCC 1051
      ||| | |||| ||| ||| || || || | ||||| ||||| | |
Db      513 GGGGTTTCCGTGTTCACTCTCACGGCCCTCAGCGCTGACAGGTACAGAGCTATCGTGAAC 572

Qy      1052 TGGAGTCGTGTTTCAGGGAATTGGGATTCCCTTTGGTAAGTCCATTGAAATTGTCTCCATC 1111
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Db      573 CCCATGGACATGCAGACGTCTGGTGTGGTGTGTGGACAGTTTGAAGGCCGTGGGCATC 632

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Qy 1112 TGGATCCTGTCCTTTATCCTGGCCATTCCCTGAAGCGATTGGCTTCGTATGGTACCCTTT 1171  
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 Db 633 TGGGTGGTCTCTGTGCTGTTGGCTGTCCCTGAGGCTGTGTTTTCGGAAGTAGCACGCATC 692  
 Qy 1172 G 1172  
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 Db 693 G 693

RESULT 15

US-08-279-590A-1

; Sequence 1, Application US/08279590A

; Patent No. 5656749

; GENERAL INFORMATION:

; APPLICANT: ELIOT R. SPINDEL, SRINIVASA

; APPLICANT: NAGALLA AND BRENDA BARRY

; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING

; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE

; TITLE OF INVENTION: PEPTIDES

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 50Z or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/279,590A

; FILING DATE: July 22, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: No. 5656749e

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Y. Rocky Tsao

; REGISTRATION NUMBER: 34,053

; REFERENCE/DOCKET NUMBER: 00537/098001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1563

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-279-590A-1

Query Match

1.5%; Score 63.6; DB 1; Length 1563;

Best Local Similarity 45.5%; Pred. No. 1.5e-06;  
Matches 332; Conservative 0; Mismatches 374; Indels 24; Gaps 2;

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Qy      735 CTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGA 794
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Qy      795 TCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCC 854
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Db      400 TATTTTTTTAAAATCAAGTCAATGCAGACTGTTCTTAATATTTTCATCACCAGCCTGGCTT 459

Qy      855 TTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTG 914
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Db      460 TTGGAGATCTTCTTCTACTGCTGACCTGCGTGCCAGTGGACGCATCTCGGTATATTGTGG 519

Qy      915 GCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTT 974
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Db      520 ACACGTGGATGTTTGAAGAGCTGGCTGT-----AAGATAATTTCCCTTCA 564

Qy      975 TGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGT 1034
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Db      565 TACAGCTTACCTCTGTCTGGAGTGTCTGGTGTCTTACTTTAACTGTCCTCAGTACTGACAGGT 624

Qy     1035 ACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCCTTTGGTAACTGCCA 1094
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Db      625 ACAGAGCCATTGTGAAACCCTTGCAATTGCAGACCTCAGATGCCGTTTTGAAGACATGTG 684

Qy     1095 TTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTCTGAAGCGATTGGCT 1154
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Db      685 GCAAAGCTGTTTGTGTTTGGATCATTCCATGCTCCTCGCTGCTCCAGAAGCTGTGTTCT 744

Qy     1155 TCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCCA 1214
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Db      745 CAGATTTGTATGAATTTGGCAGCTCGGAAAAAATACCACCTTTTGAAGCCTGTGCTCCAT 804

Qy     1215 CATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTCTATT 1274
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Db      805 ATCCAGTCTCTGAAAAGATTCTGCAAGAGACACATTCCCTAATATGCTTCCTGGTATTCT 864

Qy     1275 TCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGA 1334
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Db      865 ACATTGTTCCCCTGTCAATCATTTCTGCATAFTACTTCCTTATTGCAAAAACCTGTACA 924

Qy     1335 A-----CAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGC 1385
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Db      925 AAAGTACTTTCAACATGCCTGCTGAAGAGCACACTCACGCCCGAAAACAGATAGAATCGC 984

Qy     1386 GTCGAGAAGTGGCAAAAACAGTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCC 1445
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Db      985 GCAAACGAGTGGCAAAAACAGTGTGTTGGTGTGTTGGTGGCATTGTTGCGAGTGTGCTGGTTGC 1044

Qy     1446 CTCTTCACTT 1455
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Db     1045 CAAACCACAT 1054

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Search completed: May 14, 2004, 15:54:32



Job time : 263.426 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 14, 2004, 10:14:36 ; Search time 1559.76 Seconds  
(without alignments)  
11943.281 Million cell updates/sec

Title: US-09-931-157-1  
Perfect score: 4105  
Sequence: 1 gaattcgcgccgcctcttg.....taaaagtttacagaaacctt 4105

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
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- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq2:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
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- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result                    %  
Query

No.	Score	Match	Length	DB	ID	Description
1	4105	100.0	4105	9	US-09-931-157-1	Sequence 1, Appli
2	4105	100.0	4105	15	US-10-225-567A-115	Sequence 115, App
3	4105	100.0	4105	15	US-10-007-926A-229	Sequence 229, App
4	4105	100.0	4105	15	US-10-101-510-370	Sequence 370, App
5	4105	100.0	4105	16	US-10-372-683-46	Sequence 46, Appl
6	4079	99.4	4079	16	US-10-305-720-1257	Sequence 1257, Ap
7	2470	60.2	2595	9	US-09-919-497-12	Sequence 12, Appl
8	2470	60.2	2595	15	US-10-204-752-30	Sequence 30, Appl
9	1280.8	31.2	1284	11	US-09-826-509-494	Sequence 494, App
10	521	12.7	560	15	US-10-101-510-59	Sequence 59, Appl
11	446.2	10.9	468	13	US-10-085-783A-41606	Sequence 41606, A
12	446.2	10.9	468	16	US-10-242-535A-41606	Sequence 41606, A
13	412.4	10.0	451	10	US-09-918-995-8960	Sequence 8960, Ap
14	395.8	9.6	1470	16	US-10-305-720-1203	Sequence 1203, Ap
15	395.8	9.6	1632	12	US-10-311-671-28	Sequence 28, Appl
16	395.8	9.6	1877	13	US-10-116-802-118	Sequence 118, App
17	395.8	9.6	4286	10	US-09-921-406C-13	Sequence 13, Appl
18	395.8	9.6	4286	15	US-10-225-567A-113	Sequence 113, App
19	395.8	9.6	4286	15	US-10-007-926A-177	Sequence 177, App
20	395.8	9.6	4286	15	US-10-210-120-15	Sequence 15, Appl
21	395.8	9.6	4286	16	US-10-372-683-48	Sequence 48, Appl
22	395.8	9.6	4301	9	US-09-931-157-2	Sequence 2, Appli
23	395.8	9.6	4305	13	US-10-116-802-116	Sequence 116, App
24	392.6	9.6	1329	11	US-09-826-509-496	Sequence 496, App
25	384.8	9.4	1892	13	US-10-116-802-117	Sequence 117, App
26	381.2	9.3	1578	13	US-10-235-192A-32	Sequence 32, Appl
27	284.4	6.9	438	9	US-09-867-701-3320	Sequence 3320, Ap
c 28	155	3.8	170	15	US-10-007-926A-228	Sequence 228, App
c 29	147	3.6	592	9	US-09-962-436-531	Sequence 531, App
c 30	147	3.6	592	9	US-09-880-107-2060	Sequence 2060, Ap
c 31	147	3.6	592	9	US-09-954-531-917	Sequence 917, App
32	114.6	2.8	800	9	US-09-778-927A-27	Sequence 27, Appl
c 33	101	2.5	183337	15	US-10-020-141-5	Sequence 5, Appli
34	100	2.4	101	10	US-09-998-904-6	Sequence 6, Appli
35	91	2.2	1155	11	US-09-826-509-510	Sequence 510, App
36	91	2.2	1726	13	US-10-342-887-1136	Sequence 1136, Ap
37	91	2.2	1726	13	US-10-172-118-1136	Sequence 1136, Ap
38	91	2.2	1726	13	US-10-388-578-9	Sequence 9, Appli
39	91	2.2	1726	15	US-10-225-567A-129	Sequence 129, App
40	91	2.2	1726	16	US-10-305-720-1215	Sequence 1215, Ap
41	79.6	1.9	1200	17	US-10-221-384-1	Sequence 1, Appli
42	79.6	1.9	1413	15	US-10-225-567A-57	Sequence 57, Appl
43	79.6	1.9	1413	16	US-10-305-720-1275	Sequence 1275, Ap
44	78	1.9	1200	11	US-09-826-509-458	Sequence 458, App
45	68.6	1.7	1173	11	US-09-826-509-530	Sequence 530, App

#### ALIGNMENTS

RESULT 1  
 US-09-931-157-1  
 ; Sequence 1, Application US/09931157  
 ; Patent No. US20020082414A1  
 ; GENERAL INFORMATION:

```
; APPLICANT: Imura, Hiroo
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Nakanishi, Shigetada
; TITLE OF INVENTION: Human Endothelin Receptor
; FILE REFERENCE: 299002032411
; CURRENT APPLICATION NUMBER: US/09/931,157
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 08/121,446
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: 07/911,684
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: JP 3-172828
; PRIOR FILING DATE: 1991-07-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4105
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (485)...(1768)
; NAME/KEY: sig_peptide
; LOCATION: (485)...(544)
; NAME/KEY: mat_peptide
; LOCATION: (545)...(1768)
US-09-931-157-1
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Query Match          100.0%; Score 4105; DB 9; Length 4105;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 GAATTCGCGGCCCGCTCTTGCGGTCCCAGAGTGGAGTGGAAGGTCTGGAGCTTTGGGAGG 60
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Db      1 GAATTCGCGGCCCGCTCTTGCGGTCCCAGAGTGGAGTGGAAGGTCTGGAGCTTTGGGAGG 60

Qy     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCT 120
        |||
Db     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCT 120

Qy    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
        |||
Db    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240
        |||
Db    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy    241 GCAGTGCCCAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300
        |||
Db    241 GCAGTGCCCAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
        |||
Db    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360

Qy    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420
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Db	361	 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	 AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	 ACCCAGCAATGGCTCAATGCACAACATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGC	780
Db	721	 CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	 AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	 AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	 TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCTTTTTCGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	 GCTGTTCCCTTTTTCGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTACAGGAATTGGGATTCC	1080
Db	1021	 TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTACAGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCCTTATCCTGGCCATTCC	1140
Db	1081	 TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCCTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	 TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260

Db	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTC	TACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC		1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC		1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA		1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA		1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG		1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG		1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAACTGTGTATAACGAAATGGACAAGAA		1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAACTGTGTATAACGAAATGGACAAGAA		1500
Qy	1501	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC		1560
Db	1501	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC		1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG		1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG		1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC		1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC		1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG		1740
Db	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG		1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT		1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT		1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC		1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC		1860
Qy	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA		1920
Db	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA		1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA		1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA		1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT		2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT		2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGG		2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGG		2100

Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTCGGAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940

Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGTCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGTCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCTACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCTACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840



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Db      3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTGTTAG 3840
Qy      3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA 3900
      |||
Db      3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA 3900
Qy      3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960
      |||
Db      3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960
Qy      3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTCAACA 4020
      |||
Db      3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTCAACA 4020
Qy      4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080
      |||
Db      4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080
Qy      4081 TAAAATAAAAAGTTTACAGAAACCTT 4105
      |||
Db      4081 TAAAATAAAAAGTTTACAGAAACCTT 4105

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# RESULT 2

US-10-225-567A-115

; Sequence 115, Application US/10225567A

; Publication No. US20030113798A1

## ; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 115

; LENGTH: 4105

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-115

Query Match 100.0%; Score 4105; DB 15; Length 4105;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60
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Db      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60

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Qy      61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCCTCCGGAGTTTTCTTTTTCGTGCGAGCCCT 120

```

Db	61	 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTCTTTTCGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCGAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	 GCAGTGCCCGAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCTCCGCGCCACCCACCTCGCTTCTCCGGCTTCCTC	360
Db	301	 CGGAGCCCGGGACACCGGCCACCTCCGCGCCACCCACCTCGCTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCGAGGCGCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	 TGGCCCGAGGCGCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCAC	600
Db	541	 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	 ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	 CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	 AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	 AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960

Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	1080
Db	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800

Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCCCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCCCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAC TGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAC TGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCAC TATTTATTTTTTTAAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCAC TATTTATTTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640

Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCAGTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCAGTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAACTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAACTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540

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Db      3481 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA 3540
Qy      3541 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT 3600
Db      3541 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT 3600
Qy      3601 TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATA 3660
Db      3601 TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATA 3660
Qy      3661 ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG 3720
Db      3661 ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG 3720
Qy      3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG 3780
Db      3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG 3780
Qy      3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG 3840
Db      3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG 3840
Qy      3841 ACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900
Db      3841 ACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900
Qy      3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960
Db      3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960
Qy      3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020
Db      3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020
Qy      4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080
Db      4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080
Qy      4081 TAAAATAAAAAGTTTACAGAAACCTT 4105
Db      4081 TAAAATAAAAAGTTTACAGAAACCTT 4105

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RESULT 3

US-10-007-926A-229

; Sequence 229, Application US/10007926A

; Publication No. US20030143539A1

; GENERAL INFORMATION:

; APPLICANT: BERTUCCI, FRANCOIS

; APPLICANT: HOULGATTE, REMI

; APPLICANT: BIRNBAUM, DANIEL

; APPLICANT: NGUYEN, CATHERINE

; APPLICANT: VIENS, PATRICE

; APPLICANT: FERT, VINCENT

; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS

; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

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; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 229
; LENGTH: 4105
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: endothelin receptor type a (EDNRA) gene.
US-10-007-926A-229

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Query Match          100.0%; Score 4105; DB 15; Length 4105;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GAATTCGCGGCCGCCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60
        |||
Db      1 GAATTCGCGGCCGCCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60

Qy     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTCGTGCGAGCCCT 120
        |||
Db     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTCGTGCGAGCCCT 120

Qy    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
        |||
Db    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240
        |||
Db    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy    241 GCAGTGCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300
        |||
Db    241 GCAGTGCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
        |||
Db    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360

Qy    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420
        |||
Db    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420

Qy    421 AAAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480
        |||
Db    421 AAAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480

Qy    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
        |||
Db    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540

Qy    541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 600
        |||

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Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440



Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTGA	2280
Db	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTGA	2280

Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCAGTATTTATTTTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCAGTATTTATTTTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCCTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCCTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAACAATTGTAAATTTCTTTTAGCCC	3180

Db	3121	 AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	 ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	 GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAACTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	 GTCTGAGCTAAAACTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	 TGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	 AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	 TGTCTGATATTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	 ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020

Db 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020

Qy 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080  
 |||

Db 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080

Qy 4081 TAAAATAAAAAGTTTACAGAAACCTT 4105  
 |||

Db 4081 TAAAATAAAAAGTTTACAGAAACCTT 4105

RESULT 4

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; APPLICANT: WANG, YIXIN

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Query Match 100.0%; Score 4105; DB 15; Length 4105;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCGCGGCCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60  
 |||

Db 1 GAATTCGCGGCCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60

Qy 61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCT 120  
 |||

Db 61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCT 120

Qy 121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180  
 |||

Db 121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy 181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240  
 |||

Db 181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy 241 GCAGTGGCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300  
 |||

Db 241 GCAGTGGCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

Qy 301 CGGAGCCCGGGACACCGGCCACCTCCGCGCCACCCACCTCGCTTTCTCCGGCTTCCTC 360

Db	301		CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361		TGGCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361		TGGCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421		AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421		AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481		CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481		CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541		CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCAC	600
Db	541		CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCAC	600
Qy	601		TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601		TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661		ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661		ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721		CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721		CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781		AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781		AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841		AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841		AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901		TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901		TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961		GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961		GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021		TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	1080
Db	1021		TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	1080
Qy	1081		TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081		TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141		TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200

Db	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACCTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACCTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040

Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880

Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTAATAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCTAATAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780





Db	1	GAATTCGCGGCCCGCCTCTTGCGGTCCCAGAGTGGAGTGGAAAGGTCTGGAGCTTTGGGAGG	60
Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCCTCCGGAGTTTCTTTTTCTGTCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCCTCCGGAGTTTCTTTTTCTGTCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCAAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCAAGGAAGTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCCCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCCCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCTGTCGACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCTGTCGACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900

Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTTCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTTCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAACAACCACAACACAGACCG	1740

Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTACAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTACAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACCTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTGTATGA	2640

Db	2581	 TTCAATCAGATAGTTCTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	 AAAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	 TCAGTGCACCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	 ATGATTTCGGAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	 CACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	 TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTT	3000
Db	2941	 GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	 TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	 GGCCACACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	 AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	 ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	 GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAACTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	 GTCTGAGCTAAAACTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	 TGTAGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480

Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Qy	4081	TAAAATAAAAGTTTACAGAAACCTT	4105
Db	4081	TAAAATAAAAGTTTACAGAAACCTT	4105

RESULT 6

US-10-305-720-1257

; Sequence 1257, Application US/10305720

; Publication No. US20040010136A1

; GENERAL INFORMATION:

; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.

; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression

; FILE REFERENCE: PA-0002-1 CON

; CURRENT APPLICATION NUMBER: US/10/305,720

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; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1257
; LENGTH: 4079
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g219649
US-10-305-720-1257
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Query Match          99.4%; Score 4079; DB 16; Length 4079;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4079; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      5 TCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGGAGAC 64
          |||
Db      1 TCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGGAGAC 60

Qy     65 GGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCTCGCG 124
          |||
Db     61 GGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCTCGCG 120

Qy    125 CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC 184
          |||
Db    121 CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC 180

Qy    185 CATCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCGGGAGAAGCAG 244
          |||
Db    181 CATCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCGGGAGAAGCAG 240

Qy    245 TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA 304
          |||
Db    241 TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA 300

Qy    305 GCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTCTGGC 364
          |||
Db    301 GCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTCTGGC 360

Qy    365 CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAA 424
          |||
Db    361 CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAA 420

Qy    425 AGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAG 484
          |||
Db    421 AGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAG 480

Qy    485 ATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT 544
          |||
Db    481 ATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT 540

Qy    545 GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCACTTTT 604
          |||
Db    541 GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCACTTTT 600
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Qy	605	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	664
Db	601	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	660
Qy	665	AGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAA	724
Db	661	AGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAA	720
Qy	725	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGCAACT	784
Db	721	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGCAACT	780
Qy	785	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
Db	781	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	840
Qy	845	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	841	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	900
Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	901	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	960
Qy	965	TTCCCCCTTTTGCAGAACTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	961	TTCCCCCTTTTGCAGAACTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1020
Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGAATTGGGATTCCTTTG	1084
Db	1021	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGAATTGGGATTCCTTTG	1080
Qy	1085	GTAAGTGGCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCCTGAA	1144
Db	1081	GTAAGTGGCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCCTGAA	1140
Qy	1145	GCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1204
Db	1141	GCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1200
Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	1201	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1260
Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1324
Db	1261	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1320
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384
Db	1321	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1380
Qy	1385	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTGCTGGTTC	1444
Db	1381	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTGCTGGTTC	1440



Qy	1445	CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGA	1504
Db	1441	CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGA	1500
Qy	1505	TGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG	1564
Db	1501	TGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG	1560
Qy	1565	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1624
Db	1561	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1620
Qy	1625	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1684
Db	1621	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1680
Qy	1685	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAACAACCACAACACAGACCGGAGC	1744
Db	1681	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAACAACCACAACACAGACCGGAGC	1740
Qy	1745	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAATC	1804
Db	1741	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAATC	1800
Qy	1805	CTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1864
Db	1801	CTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1860
Qy	1865	TTCCTTAATTCCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1924
Db	1861	TTCCTTAATTCCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1920
Qy	1925	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1984
Db	1921	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1980
Qy	1985	GCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2044
Db	1981	GCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2040
Qy	2045	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2104
Db	2041	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2100
Qy	2105	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAGAGAT	2164
Db	2101	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAGAGAT	2160
Qy	2165	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2224
Db	2161	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2220
Qy	2225	GGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTGCATAAT	2284
Db	2221	GGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTGCATAAT	2280
Qy	2285	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAAAATA	2344

Db	2281	 AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAATA	2340
Qy	2345	GTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTTTAAAACAC	2404
Db	2341	 GTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTTTAAAACAC	2400
Qy	2405	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2464
Db	2401	 AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2460
Qy	2465	GCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2524
Db	2461	 GCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2520
Qy	2525	TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTCA	2584
Db	2521	 TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTCA	2580
Qy	2585	ATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAAA	2644
Db	2581	 ATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAAA	2640
Qy	2645	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCAG	2704
Db	2641	 TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCAG	2700
Qy	2705	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2764
Db	2701	 TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2760
Qy	2765	TTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2824
Db	2761	 TTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2820
Qy	2825	TCCTATTCTCTTAATTTTTGTGTTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2884
Db	2821	 TCCTATTCTCTTAATTTTTGTGTTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2880
Qy	2885	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2944
Db	2881	 CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2940
Qy	2945	AATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTTCAG	3004
Db	2941	 AATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTTCAG	3000
Qy	3005	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCACCATTTCAAAGGGCC	3064
Db	3001	 TATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCACCATTTCAAAGGGCC	3060
Qy	3065	CACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3124
Db	3061	 CACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3120
Qy	3125	TC'TTTTACTAGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATTT	3184

Db	3121	TCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATTT	3180
Qy	3185	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3244
Db	3181	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3240
Qy	3245	TGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCT	3304
Db	3241	TGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCT	3300
Qy	3305	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3364
Db	3301	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3360
Qy	3365	GCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3424
Db	3361	GCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3420
Qy	3425	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3484
Db	3421	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3480
Qy	3485	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3544
Db	3481	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3540
Qy	3545	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3604
Db	3541	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3600
Qy	3605	TGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3664
Db	3601	TGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3660
Qy	3665	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3724
Db	3661	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3720
Qy	3725	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3784
Db	3721	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3780
Qy	3785	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3844
Db	3781	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3840
Qy	3845	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATTC	3904
Db	3841	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATTC	3900
Qy	3905	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3964
Db	3901	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3960
Qy	3965	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA	4024
Db	3961	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA	4020

Qy 4025 ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTAA 4083  
|||||  
Db 4021 ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTAA 4079

RESULT 7

US-09-919-497-12

; Sequence 12, Application US/09919497

; Patent No. US20020106662A1

; GENERAL INFORMATION:

; APPLICANT: Mutter, George L.

; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER

; FILE REFERENCE: B0801/7225

; CURRENT APPLICATION NUMBER: US/09/919,497

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: US 60/221,735

; PRIOR FILING DATE: 2000-07-31

; NUMBER OF SEQ ID NOS: 100

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 12

; LENGTH: 2595

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-919-497-12

Query Match 60.2%; Score 2470; DB 9; Length 2595;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1624 CCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCAT 1683  
|||||  
Db 15 CCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCAT 74

Qy 1684 GAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG 1743  
|||||  
Db 75 GAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG 134

Qy 1744 CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT 1803  
|||||  
Db 135 CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT 194

Qy 1804 CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT 1863  
|||||  
Db 195 CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT 254

Qy 1864 CTTCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG 1923  
|||||  
Db 255 CTTCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG 314

Qy 1924 GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC 1983  
|||||  
Db 315 GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC 374

Qy 1984 TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA 2043  
|||||  
Db 375 TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA 434

Qy	2044	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTA	2103
Db	435	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTA	494
Qy	2104	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAAACTTTAGAGA	2163
Db	495	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAAACTTTAGAGA	554
Qy	2164	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2223
Db	555	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614
Qy	2224	TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	2283
Db	615	TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	2343
Db	675	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAAACA	2403
Db	735	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAAACA	794
Qy	2404	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	GGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	2583
Db	915	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTACAAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	AATCAGATAGTTCTTTTTTACAAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	2763
Db	1094	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	1153
Qy	2764	ATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	ATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	2883
Db	1214	CTCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	1273

Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	2943
Db	1274	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTCA	3003
Db	1334	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	3063
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
Db	1694	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	1753
Qy	3364	AGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	AGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	3483
Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	3543
Db	1874	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	3663
Db	1994	CTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	2053
Qy	3664	TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	3723
Db	2054	TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCGCAT	3783

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Db      2114  |||||GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCTGGCGCAT 2173
Qy      3784  CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA 3843
Db      2174  |||||CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA 2233
Qy      3844  ATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATT 3903
Db      2234  |||||ATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATT 2293
Qy      3904  CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA 3963
Db      2294  |||||CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA 2353
Qy      3964  CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 4023
Db      2354  |||||CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 2413
Qy      4024  AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA 4083
Db      2414  |||||AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA 2473
Qy      4084  AATAAAAGTTTACAGAAACCTT 4105
Db      2474  |||||AATAAAAGTTTACAGAAACCTT 2495

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RESULT 8

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US-10-204-752-30
; Sequence 30, Application US/10204752
; Publication No. US20030152956A1
; GENERAL INFORMATION:
; APPLICANT: OHTANI, No. US20030152956Alike
; APPLICANT: MATSUI, Keiko
; APPLICANT: YOSHIDA, Nei
; APPLICANT: SUGITA, Yuji
; APPLICANT: IZUHARA, Kenji
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASE
; FILE REFERENCE: SHZ-009US
; CURRENT APPLICATION NUMBER: US/10/204,752
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: JP 2000-396166
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-204-752-30

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Query Match          60.2%;  Score 2470;  DB 15;  Length 2595;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 2481;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 1;

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Qy      1624  CCAGTCATGCCTCTGCTGCTGCTGTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCAT 1683

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Db	15		CCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCAT	74
Qy	1684		GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG	1743
Db	75		GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG	134
Qy	1744		CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	1803
Db	135		CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	194
Qy	1804		CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT	1863
Db	195		CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT	254
Qy	1864		CTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCAAAACCGCAAGGTAGACTG	1923
Db	255		CTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCAAAACCGCAAGGTAGACTG	314
Qy	1924		GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	1983
Db	315		GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	374
Qy	1984		TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTAAA	2043
Db	375		TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTAAA	434
Qy	2044		TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAGTACATGGCTA	2103
Db	435		TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAGTACATGGCTA	494
Qy	2104		GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTAGAGA	2163
Db	495		GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTAGAGA	554
Qy	2164		TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2223
Db	555		TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614
Qy	2224		TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTGCATAA	2283
Db	615		TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTGCATAA	674
Qy	2284		TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAAAAT	2343
Db	675		TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAAAAT	734
Qy	2344		AGTATTCAGGTGAGCAATTAGATTAGTATTTCCACGTCACCTATTTATTTTTTTAAAACA	2403
Db	735		AGTATTCAGGTGAGCAATTAGATTAGTATTTCCACGTCACCTATTTATTTTTTTAAAACA	794
Qy	2404		CAAATTCATAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795		CAAATTCATAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464		GGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523



Db	855	GGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	2583
Db	915	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTACAAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	AATCAGATAGTTCTTTTTTACAAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATG	2763
Db	1094	GTGCACTGTATATAGAAGTCTAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATG	1153
Qy	2764	ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTGTTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	2883
Db	1214	CTCCTATTCTCTTAATTTTTGTTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	2943
Db	1274	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	AAATAATTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	3063
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCAT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCAT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
Db	1694	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	1753

Qy	3364	AGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	AGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	3483
Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	3543
Db	1874	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAAATT	3663
Db	1994	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAAATT	2053
Qy	3664	TGTTGGGCCATATTTTAGGACAGGTAATAAACATCAGGTTCCAGTTGCTTGAATTGCAA	3723
Db	2054	TGTTGGGCCATATTTTAGGACAGGTAATAAACATCAGGTTCCAGTTGCTTGAATTGCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCGCAT	3783
Db	2114	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCGCAT	2173
Qy	3784	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	3843
Db	2174	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	2233
Qy	3844	ATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATT	3903
Db	2234	ATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATT	2293
Qy	3904	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	3963
Db	2294	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	2353
Qy	3964	CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT	4023
Db	2354	CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT	2413
Qy	4024	AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA	4083
Db	2414	AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA	2473
Qy	4084	AATAAAAGTTTACAGAAACCTT	4105
Db	2474	AATAAAAGTTTACAGAAACCTT	2495

RESULT 9

US-09-826-509-494

; Sequence 494, Application US/09826509



Db	421	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	480
Qy	965	TTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	481	TTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	540
Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGGAATTGGGATTCCTTTG	1084
Db	541	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGGAATTGGGATTCCTTTG	600
Qy	1085	GTAAGTCCCATTTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1144
Db	601	GTAAGTCCCATTTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	660
Qy	1145	GCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1204
Db	661	GCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	720
Qy	1205	CTCAATGCCACATCAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	721	CTCAATGCCACATCAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	780
Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1324
Db	781	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	840
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384
Db	841	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	900
Qy	1385	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTC	1444
Db	901	CGTCGAGAAGTGAACAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTC	960
Qy	1445	CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGA	1504
Db	961	CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGA	1020
Qy	1505	TGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAAGTGGCAACCATG	1564
Db	1021	TGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAAGTGGCAACCATG	1080
Qy	1565	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1624
Db	1081	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1140
Qy	1625	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCATG	1684
Db	1141	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCATG	1200
Qy	1685	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1744
Db	1201	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1260
Qy	1745	AGCCATAAGGACAGCATGAACTGA	1768
Db	1261	AGCCATAAGGACAGCATGAACTGA	1284

RESULT 10

US-10-101-510-59

; Sequence 59, Application US/10101510  
 ; Publication No. US20030148295A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WAN, JACKSON  
 ; APPLICANT: WANG, YIXIN  
 ; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE  
 ; FILE REFERENCE: 15117.0012  
 ; CURRENT APPLICATION NUMBER: US/10/101,510  
 ; CURRENT FILING DATE: 2002-03-20  
 ; PRIOR APPLICATION NUMBER: 60/276,947  
 ; PRIOR FILING DATE: 2001-03-20  
 ; NUMBER OF SEQ ID NOS: 805  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 59  
 ; LENGTH: 560  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-101-510-59

Query Match 12.7%; Score 521; DB 15; Length 560;  
 Best Local Similarity 97.7%; Pred. No. 4e-120;  
 Matches 550; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

Qy	2464	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	1	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	60
Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	2583
Db	61	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	120
Qy	2584	AATCAGATAGTTCTTTTTTACAAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	121	AATCAGATAGTTCTTTTTTACAAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	179
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	2703
Db	180	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	239
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATG	2763
Db	240	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATG	299
Qy	2764	ATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	300	ATTCGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	359
Qy	2824	CTCCTATTCTCTTAATTTTTGTTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	2883
Db	360	CTCCTATTCTCTTAATTTTTCTTAAATGTTAACTGGCAGTAAAGCTTTTTTGATCATTC	419
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTGAGTGAA	2943

Db 420 CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA 479

Qy 2944 AAATAATTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACTTCTTGGGGTTTTCA 3003  
 |||| | |||||||||||| |||| | | |||||||||||||||||||||||||

Db 480 AAATAATACCCACAAATGGCACCAG--AACTTACGATTCTTCACTTCTTGGGGTTTTCA 537

Qy 3004 GTATGAACCTAACTCCCCACCCC 3026  
 ||||||||||||||||

Db 538 GTATGAACCTAACTCCCCACCCC 560

RESULT 11

US-10-085-783A-41606  
 ; Sequence 41606, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; APPLICANT: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085,783A  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/305,340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: US 60/275,017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIOR APPLICATION NUMBER: US 60/271,955  
 ; PRIOR FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 41606  
 ; LENGTH: 468  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (12)..(12)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (415)..(415)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 US-10-085-783A-41606

Query Match 10.9%; Score 446.2; DB 13; Length 468;  
 Best Local Similarity 97.8%; Pred. No. 2.3e-101;  
 Matches 451; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 3573 ATTCAATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACA 3632  
 | | ||||||||||||||||||||||||||||||||||||||||||||

Db 8 AATTNATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACA 67

Qy 3633 GATTGCTGATAATAAATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAA 3692  
 ||||||||||||||||||||||||||||||||||||||||||||

Db 68 GATTGCTGATAATAAATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAA 127

Qy 3693 TAACATCAGGTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTT 3752

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Db      128 TAACATCAGGTTCCAGTTGCTTGAATTACAAGGCTAAGAAGTACTGCCCTTTTGTGTGTT 187
Qy      3753 AGCAGTCAAATCTATTATTCCACTGGCGCATCATATGCAGTGATATATGCCCTATAATATA 3812
Db      188 AGCAGTCAAATCTATTATTCCACTGGCGCATCATATGCAGTGATATATGCCCTATAATATA 247
Qy      3813 AGCCATAGGTTACACCATTTTGTGTTAGACAATTGTCTTTTTTTTCAAGATGCTTTGTGTTTC 3872
Db      248 AGCCATAGGTTACACCATTTTGTGTTAGACAATTGTCTTTTTTTTCAAGATGCTTTGTGTTTC 307
Qy      3873 TTTCATATGAAAAAATGCATTTTATAAATTCAGAAAGTCATAGATTTCTGAAGGCGTCA 3932
Db      308 TTTCATATGAAAAAATGCATTTTATAAATTCAGAAAGTCATAGATTTCTGAAGGCGTCA 367
Qy      3933 ACGTGCATTTTATTTATGGACTGGTAAGTAAGTGTGGTTTACTAGCAGGAATATTTCCAA 3992
Db      368 ACGTGCATTTTATTTATGGACTGGTAAGTACTGGGGGGTTACTAGCANGAATATTTCCAA 427
Qy      3993 TTTCTACCTTTACTACATCTTTTCAACAAGTAAGTTGTAG 4033
Db      428 TTTCTACCTTTACTACATCTTTTCAACAAGTAAGTTGTAG 468

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RESULT 12

US-10-242-535A-41606

; Sequence 41606, Application US/10242535A

; Publication No. US20040013663A1

; GENERAL INFORMATION:

; APPLICANT: ChondroGene Inc.

; APPLICANT: Liew, C.C.

; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis

; FILE REFERENCE: 4231/2005

; CURRENT APPLICATION NUMBER: US/10/242,535A

; CURRENT FILING DATE: 2002-09-12

; PRIOR APPLICATION NUMBER: US 10/085,783

; PRIOR FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/305,340

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/275,017

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: US 60/271,955

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 58994

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 41606

; LENGTH: 468

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (12)..(12)

; OTHER INFORMATION: n is a, c, g, or t

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (415)..(415)

; OTHER INFORMATION: n is a, c, g, or t





US-09-918-995-8960

Matches 416; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3767 TT 3768

11

US-10-305-720-1203

; Publication No. US20040010136A1

; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.

FILE REFERENCE: PA-0002-1 CON

; CURRENT FILING DATE: 2002-11-26

; PRIOR FILING DATE: 1998-01-30

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; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1203
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g182275
US-10-305-720-1203

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Query Match          9.6%; Score 395.8; DB 16; Length 1470;
Best Local Similarity 65.7%; Pred. No. 2.7e-88;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

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Qy      689 TGCCACAGCAGACTAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748
      |||| | | | | | | | | | | | | | | | | | | | | | |
Db      314 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCTGC 373

Qy      749 ACTATTTTCATCGTGGGAATGGTGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808
      | | ||| | | ||| | | | |||| | | | | | | | | | |
Db      374 CTTGTGTTCTGCTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 433

Qy      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC 868
      || | | ||| | | | | | | | | | | | | | | | | | |
Db      434 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 493

Qy      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928
      | | | | | | | | | | | | | | | | | | | | | |
Db      494 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 549

Qy      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTGCAGAAGTCCTCG 988
      |||| | | | | | | | | | | | | | | | | | | | |
Db      550 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC 598

Qy      989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1048
      |||| | | | | | | | | | | | | | | | | | | | |
Db      599 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 658

Qy      1049 TCCTGGAGTCGTGTTTCAAGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCC 1108
      || | | | | | | | | | | | | | | | | | | | | |
Db      659 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 718

Qy      1109 ATCTGGATCCTGTCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATGGTACCC 1168
      || ||| | | | | | | | | | | | | | | | | | | |
Db      719 ATTTGGGTGGTCTCTGTGTTCTGGCTGTCCCTGAAGCCATAGTTTTGATATAATTACG 778

Qy      1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222
      | | | | | | | | | | | | | | | | | | | | | |
Db      779 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAAGACAGCT 838

Qy      1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1282
      |||| | | | | | | | | | | | | | | | | | | | |
Db      839 TTCATGCAGTTTACAAAGACAGCAAAAGATTGGTGGCTGTTGAGTTTCTATTTCTGCTTG 898

Qy      1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342
      || |||| | | | | | | | | | | | | | | | | | |

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Db 899 CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG 955  
 Qy 1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402  
 || | ||| || |||| | | || | || |||| | || |||| || ||  
 Db 956 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1015  
 Qy 1403 ACAGTTTTCTGCTTGCTTGTAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT 1462  
 || || || || || || | | |||| | |||| | || |||| | || |  
 Db 1016 ACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGG 1075  
 Qy 1463 ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522  
 || |||| || | |||| | | || || |||| || | | || ||  
 Db 1076 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTTT 1135  
 Qy 1523 TTAAGTCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC 1582  
 | || | |||| || || |||| || || || | |||| || || ||||  
 Db 1136 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1195  
 Qy 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642  
 || |||| |||| || |||| | || |||| || || || |||| || || ||||  
 Db 1196 ATTGCTCTGTATTTGGTGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC 1255  
 Qy 1643 TGCTG 1647  
 || ||  
 Db 1256 TGGTG 1260

# RESULT 15

US-10-311-671-28

; Sequence 28, Application US/10311671

; Publication No. US20040072996A1

## ; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: LAL, Preeti G.

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: HAFALIA, April J. A.

; APPLICANT: NGUYEN, Danniel B.

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: KALLICK, Deborah A.

; APPLICANT: GRIFFIN, Jennifer A.

; APPLICANT: YUE, Henry

; APPLICANT: KHAN, Farrah A.

; APPLICANT: ARVIZU, Chandra S.

; APPLICANT: LU, Dyung Aina M.

; APPLICANT: TRIBOULEY, Catherine M.

; APPLICANT: LU, Yan

; APPLICANT: CHAWLA, Narinder K.

; APPLICANT: GRAUL, Richard

; APPLICANT: YAO, Monique G.

; APPLICANT: YANG, Junming

; APPLICANT: RAMKUMAR, Jayalaxmi

; APPLICANT: AU-YOUNG, Janice K.

; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: HERNANDEZ, Roberto

; APPLICANT: WALSH, Roderick T.

; APPLICANT: BOROWSKY, Mark L.

; APPLICANT: THORNTON, Michael B.

```

; APPLICANT: HE, Ann
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0131 USN
; CURRENT APPLICATION NUMBER: US/10/311,671
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/19275
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,483
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/213,954
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/215,209
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 60/216,595
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,936
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/219,154
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/220,141
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 1632
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 6792419CB1
US-10-311-671-28

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Query Match          9.6%; Score 395.8; DB 12; Length 1632;
Best Local Similarity 65.7%; Pred. No. 2.9e-88;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

```

```

Qy      689 TGCCACAGCAGACTAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      555 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCTGC 614

Qy      749 ACTATTTTCATCGTGGGAATGGTGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      615 CTTGTGTTCTGCTGCTGGGGATCATCGGGAACCCACACTTCTGAGAATTATCTACAAGAAC 674

Qy      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC 868
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      675 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 734

Qy      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTT 928
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      735 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----- 790

Qy      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTGCAGAAGTCCTCG 988
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      791 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC 839

Qy      989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1048

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Db	840	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	899
Qy	1049	TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCTTTGGTAACTGCCATTGAAATTGTCTCC	1108
Db	900	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	959
Qy	1109	ATCTGGATCCTGTCCCTTTATCCTGGCCATTCCCTGAAGCGATTGGCTTCGTCATGGTACCC	1168
Db	960	ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	1019
Qy	1169	TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA	1222
Db	1020	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCCTTCAGAAGACAGCT	1079
Qy	1223	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG	1282
Db	1080	TTCATGCAGTTTACAAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTTG	1139
Qy	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
Db	1140	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG	1196
Qy	1343	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Db	1197	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA	1256
Qy	1403	ACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTCTTCACTTAAGCCGT	1462
Db	1257	ACCGTCTTTTGCCCTGGTCCCTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACTCAGCAGG	1316
Qy	1463	ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1317	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTGTAGCTTT	1376
Qy	1523	TTACTGCTCATGGATTACATCGGTATTAACTTGGCAACCATGAATTCATGTATAAACCCC	1582
Db	1377	CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA	1436
Qy	1583	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC	1642
Db	1437	ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC	1496
Qy	1643	TGCTG 1647	
Db	1497	TGGTG 1501	

Search completed: May 15, 2004, 00:12:28  
Job time : 1572.76 secs